

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 23, 2003, 09:38:24 ; Search time 43 Seconds

(without alignments)
815.030 Million cell updates/sec

Title: US-09-503-387-3

Perfect score: 1786

Sequence: 1 MSBSTALFCLGLGRVPA.....KSHGQDGRQDVHSRGLCS 339

Scoring table: R:OSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR76: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1786	100.0	339	JC7509	glycoprotein VI-1
2	428.5	24.0	466	JC5897	killer cell inhibi
3	426.5	23.9	264	I46020	FC gamma 2 recepto
4	392	21.9	287	JH0332	IGA (Fc) receptor,
5	372.5	20.9	841	JC5894	killer cell inhibi
6	358.5	20.5	635	JC5896	killer cell inhibi
7	358.5	20.1	239	JC2630	Fc alpha-1 human
8	358.5	20.0	680	JC5895	killer cell inhibi
9	335	18.9	444	G11925	KIR (cl-11) NK rec
10	330	18.5	296	553434	cell surface glyco
11	328	18.4	348	A56247	natural killer cel
12	327	18.3	444	G11924	KIR (cl-2) NK rece
13	323.5	18.1	341	I61725	natural killer ass
14	322	18.0	1327	TC9402	immunoglobulin-1ix
15	317.5	17.9	335	A53434	cell surface glyco
16	316	17.7	455	G11923	KIR (cl-5) NK rece
17	315	17.6	427	G12034	killer cell inhibi
18	289.5	16.2	303	A43807	membrane glycopro
19	182	13.2	164	T46433	hypothetical prote
20	145	8.1	237	A42013	alpha-1-3-glycopro
21	142.5	8.0	474	CMHUB	heparan sulfate pr
22	126.5	7.1	3707	S18252	Fc gamma RIIB-a.p
23	124.5	7.0	267	I56110	Fc gamma (19G) rec
24	8.5	6.6	267	A35902	perlecan precursor
25	8.5	6.6	4391	A38096	microtubule-associ
26	6.5	6.5	2774	A13359	Fc gamma (19G) rec
27	6.4	6.4	283	FCMSG	Bravo/Nr-CAN cell
28	6.4	6.4	1259	A43425	hypothetical prote
29	6.4	6.4	592	D70863	

30	113.5	6.4	1268	1	A33640	neural cell adesi
31	110.5	6.2	1612	2	T30805	ductil protein - FC
32	110	6.2	270	2	A34636	Fc-gamma receptor
33	109.5	6.1	4162	2	T42633	connectin/titin -
34	108	6.0	257	2	S03682	IGF Fc receptor a
35	107	6.0	261	2	S29360	Fc gamma (19G) rec
36	106.5	6.0	3375	2	T19821	hypothetical prote
37	106	5.9	285	2	S36903	Fc gamma (19G) rec
38	106	5.9	739	2	JN0581	vascular cell adhe
39	106	5.9	931	2	T49710	related to glucan
40	106	5.9	1607	2	T02837	long chain fatty a
41	105.5	5.9	330	2	A40071	Fc gamma (19G) rec
42	105.5	5.9	330	2	I49660	Fc gamma-1/gamma-2
43	104.5	5.9	267	2	I72882	Fc gamma receptor
44	104.5	5.9	1651	2	T14160	transmembrane rece
45	104	5.8	1367	1	S48478	glucan 1,4-alpha-g

ALIGNMENTS

RESULT 1

JC7509

glycoprotein VI-1 - human

Species: Homo sapiens (man)

Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001

Accession: JC7509; PC7101

Rezumt, Y.; Uchiyama, T.; Takayama, H.

Biochem. Biophys. Res. Commun. 277, 27-36, 2000

Title: Molecular cloning, genomic structure, chromosomal localization, and alterna

Accession: JC7509; M01D:20483673; PMID:11027634

Contents: Platelet

Accession: JC7509

Molecule type: mRNA

Residues: 1-339 <EZU>

Cross-references: DDBJ:AB043819

Accession: PC7101

Molecule type: protein

Residues: 28-41/62-79/114-142 <EZ2>

Comment: This protein, which belongs to the immunoglobulin superfamily, is the ma

or gamma chain as a signal transducing subunit, and plays some roles in cancer cells

Citations:

Gene: gpVI-1

Map position: 19q13.4

Introns: 62/11/95/11/353/11/692/11/752/11/803/1

Keywords: glycoprotein; immunoglobulin; platelet

Query Match 100.0% Score 1786; DB 2; Length 339;

Best Local Similarity 100.0% Pred. No. 8.1e-123;

Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy	1	MSBSTALFCLGLGRVPAQSGFLPKPSLQALPSSLVPLEKPYTRCGGPGVDLYRJE	60
Es	1	MSBSTALFCLGLGRVPAQSGFLPKPSLQALPSSLVPLEKPYTRCGGPGVDLYRJE	60
Cy	61	KLSSSRYQDQAVLFIAPKRSLLAGRYRCSYQNGSLKSLPSQGLFVATGVPAKPSLSACP	120
Es	61	KLSSSRYQDQAVLFIAPKRSLLAGRYRCSYQNGSLKSLPSQGLFVATGVPAKPSLSACP	120
Cy	121	SPAVSSGGDVTLQCCQTRYGFDQALYKGGPAPAYKNPBRWYRASPPTITVTAHSGTYRC	180
Es	121	SPAVSSGGDVTLQCCQTRYGFDQALYKGGPAPAYKNPBRWYRASPPTITVTAHSGTYRC	180
Cy	181	YSFSSRDPLYKASPSDPLELVVGTSTVPSRLPTEPPSSVAEFSSEATBELTVSTNKVFT	240
Es	181	YSFSSRDPLYKASPSDPLELVVGTSTVPSRLPTEPPSSVAEFSSEATBELTVSTNKVFT	240
Cy	241	TEISRSITTSFKESDSPAGPARQYTKGNLVRICLGAVILITLAGFLAEDWHSRRKRLRH	300
Es	241	TEISRSITTSFKESDSPAGPARQYTKGNLVRICLGAVILITLAGFLAEDWHSRRKRLRH	300
Cy	301	RGRVQPLPLPLPPLPQTRKSHGQDGRQDVHSRGLCS	339
Es	301	RGRVQPLPLPLPPLPQTRKSHGQDGRQDVHSRGLCS	339

Ds 301 KGRAVQRPPLPPEFQTRKSHGGQDGGKQDVHSGGCS 339

RESULT 2

CC5897

killer cell inhibitory receptor p31 precursor - human

C/Species: Homo sapiens (man)

C/Date: 16-Mar-1996 #sequence_revision 18-Mar-1998 #text_change 05-Nov-1999

C/Accession: J05897

R/Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.; Ohya

C/Biochem. 123, 358-368, 1998

A/Title: Genomic structures and chromosomal location of p31, a novel murine regulatory

A/Reference number: J05894; MUID:98218758; PMID:9538215

A/Accession: J05897

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-466 <YAY>

A/Cross-references: GB:AF041034; NID:G2791689; PIDN:AA596926.1; PID:G2791690

C/Comment: This protein function as inhibitory cell-surface molecule against cell activa

C/Genetics:

A/Map position: 19q13.3-13.4

F1-23/Domain: signal sequence #status predicted <SIG>

Query Match

Best Local Similarity 24.0%; Score 428.5; Ds 2; Length 466;

Best Local Similarity 36.1%; Pred. No. 9.1e-24;

Matches 126; Conservative 43; Mismatches 127; Indels 53; Gaps 13;

QY 1 MSPSPALFCGLG-RVPAQSGPLPKPS:QALPSS:VPLKPYTLRCQSPGVGVD--- 56

Ds 1 MTPILTLVLCGLG:GPRTHVQAGHLPKPTLMAEPGSVTLQSSPVTLRCCSLQAEVHL 60

QY 57 YRLKCSS--SRVQD---QAVLFIPAKRS:LAGRYCSYQNSLMS:PSDQJELVATGVF 111

Ds 61 YRENKASAWNRIOEPKNGCFIPSTNEHGRYHCQYVSHMSSEYSPJELVATGVF 120

QY 112 AKPSLSAQGPRAVSSGGVTLQCCQTRVGFQDALYKSGFPAPYKNPRA-----YR 162

Ds 121 SKPTLSALPSPVTLGGVTLQCVSQVAFDGFLLCKEGED---EHQRLNKHSHKRGSSR 177

QY 163 ASFPITVTAASGTVCYSSSRDPYLSASDPLEJVTGTSVTPSRLPTEFFSSVAE 222

Ds 178 AIFSVPVSPNRAWSHRCTGYDLNSPYWSSPSDLELLVPGVSKKPS-LSVQGPVWAP 236

QY 223 FSEATAEET--VSFTNKVFTTETSRISITSPKESDSPAGPARQVYTKMVAET----- 274

Ds 237 GSELTLCQVSDVGRFVLKESGRDLRQLPGRQPC-AQ:SQANFTLGPSVRSYGGQVRC 295

QY 275 LGAVTIIILAGFLAEDWHSRKRRLRHGRVAVCPPLPPLPQTRKSHG 323

Ds 296 YGAY-----NLSSEKSA-----PSCLPLDIL-ITGQIRHG 322

RESULT 3

I46020

FC gamma 2 receptor precursor - bovine

C/Species: Bos primigenius taurus (cattle)

C/Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 05-Nov-1999

C/Accession: I46020; S53115

R/Zhang, G.; Young, C.R.; Tregaskes, C.A.; Scpp, P.; Howard, C.J.

J. Immunol. 155, 1534-1541, 1995

A/Title: Identification of a novel class of mammalian FC gamma receptor.

A/Reference number: I46020; MUID:95363119; PMID:7636215

A/Accession: I46020

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-264 <ZHA>

A/Cross-references: EMBL:237506; NID:G732571; PIDN:CAA85736.1; PID:G732572

C/Keywords: immunoglobulin receptor

Query Match

Best Local Similarity 23.9%; Score 426.5; Ds 2; Length 264;

Best Local Similarity 32.5%; Pred. No. 6.5e-24;

Matches 112; Conservative 37; Mismatches 87; Indels 109; Gaps 9;

QY 1 MSPSPALFCGLG-RVPAQSGPLPKPS:QALPSS:VPLKPYTLRCQSPGVGVD--- 56

Ds 1 MTPILTLVLCGLG:GPRTHVQAGHLPKPTLMAEPGSVTLQSSPVTLRCCSLQAEVHL 60

QY 57 YRLKCSS--SRVQD---QAVLFIPAKRS:LAGRYCSYQNSLMS:PSDQJELVATGVF 111

Ds 61 YRENKASAWNRIOEPKNGCFIPSTNEHGRYHCQYVSHMSSEYSPJELVATGVF 120

QY 112 AKPSLSAQGPRAVSSGGVTLQCCQTRVGFQDALYKSGFPAPYKNPRA-----YR 162

Ds 121 SKPTLSALPSPVTLGGVTLQCVSQVAFDGFLLCKEGED---EHQRLNKHSHKRGSSR 177

QY 163 ASFPITVTAASGTVCYSSSRDPYLSASDPLEJVTGTSVTPSRLPTEFFSSVAE 222

Ds 178 AIFSVPVSPNRAWSHRCTGYDLNSPYWSSPSDLELLVPGVSKKPS-LSVQGPVWAP 236

QY 223 FSEATAEET--VSFTNKVFTTETSRISITSPKESDSPAGPARQVYTKMVAET----- 274

Ds 237 GSELTLCQVSDVGRFVLKESGRDLRQLPGRQPC-AQ:SQANFTLGPSVRSYGGQVRC 295

QY 275 LGAVTIIILAGFLAEDWHSRKRRLRHGRVAVCPPLPPLPQTRKSHG 323

Ds 296 YGAY-----NLSSEKSA-----PSCLPLDIL-ITGQIRHG 322

QY 1 MSPSPALFCGLG-RVPAQSGPLPKPS:QALPSS:VPLKPYTLRCQSPGVGVD 59

Ds 1 MTPILTLVLCGLG:GPRTHVQAGHLPKPTLMAEPGSVTLQSSPVTLRCCSLQAEVHL 60

QY 60 EKLSSS-----RYCQAVLFIPAKRS:LAGRYCSYQNSLMS:PSDQJELVATG- 109

Ds 61 NKEGDS:TPWNHPSLEFPCXANFFISNVREQAGRYHCHSHFIGNMSEPSPEJDLVAGE 120

QY 110 -----VFAKPSLSAQGPRAVSSGGVTLQCCQTRVGFQDALYKSG---DEAPYKNPRA- 159

Ds 121 EPAGRLDRPSTSVRFPSPVAVGENTLLCQSNRTDFTLSKEGAHPRPLRFSQDQDQ 160

QY 160 WPAASFPITVTAASGTVCYSSSRDPYLSASDPLEJVTGTSVTPSRLPTEPPSS 219

Ds 181 WYQAEFS:SPVTSAHGTYRCYRSLSTNPVLLSQPSSEPLALVAD----- 225

QY 220 VAEFSEATAELTVSFTNKVFTTETSRISITSPKESDSPAGPARQVYTKNLVRLCQAVI 279

Ds 226 -----YTXQLIRMSGLAASV 240

QY 280 LILVAGFLAEDWHSRKRRLRHGRVAVCPPLPPLPQTRKSHG 324

Ds 241 LLLV-GLV-----LQARHDSG 257

RESULT 4

CH0332

Iga (Fc) receptor, myeloid cell (CD89) precursor - human

A/Alternate names: myeloid glycoprotein CD89

C/Species: Homo sapiens (man)

C/Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-Nov-1999

C/Accession: JH0332; I37224; S14435

R/Maliszewski, C.R.; March, C.C.; Schoenborn, Y.A.; Gimpey, S.; Shen, L.

J. Exp. Med. 172, 1665-1672, 1993

A/Title: Expression cloning of a human Fc receptor for IgA.

A/Reference number: CH0332; MUID:91079769; PMID:2258698

A/Accession: JH0332

A/Molecule type: mRNA

A/Residues: 1-287 <MAL>

A/Cross-references: GB:X54150; NID:G11329; PIDN:CAA38089.1; PID:G11330

A/Experimental source: myeloid cell liver V937

A/Introns: 12/1; 24/1; 121/1; 217/1

A/Keywords: glycoprotein; immunoglobulin receptor; transmembrane protein

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-287/Product: Iga receptor Fc alpha #status predicted <MFC>

F:228-246/Domain: transmembrane #status predicted <TRA>

F:65,79,141,177,186/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 21.9%; Score 392; Ds 2; Length 287;

Best Local Similarity 31.2%; Pred. No. 2.3e-21;

Matches 100; Conservative 43; Mismatches 110; Indels 68; Gaps 5;

QY 1 MSPSPALFCGLG-RVPAQSGPLPKPS:QALPSS:VPLKPYTLRCQSPGVGVD 59

Ds 1 MTPILTLVLCGLG:GPRTHVQAGHLPKPTLMAEPGSVTLQSSPVTLRCCSLQAEVHL 60

QY 60 EKLSSSRYQD-----QAVLFIPAKRS:LAGRYCSYQNSLMS:PSDQJELVAT 108

Ds 61 WIKNSTYREIGRLKFWNETDEPFVTDHMDANAGRYCCQYRIGHYRFRYSDELVAT 120

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QY 109 GFAPKPSLSAGPGPAVSSGGVTLQCCTRY-GFDQFALYKSDPAFYKPERWYRASFF 167
DB 121 GLYGKPFJLSADRGVLMPEGNISLTCCSAHIFDFRSLAKGELSLPQHGGEPANFSL 180
QY 168 ITVTAAHSGTYRCYCSFSSRCQPYLMSAPSDPELVYTGTSVTPSRLLPTEPPSSVAEFSSEAT 227
DB 191 GPVLDLWVGTYRCYGYWYNRSPYQWSPSNALDEAVT----- 216
QY 228 AELTVSFTNKVFTTETSRSLTSPKESDSPAGEARQYTYTKGRVPRICLGAVTTLAAGFL 287
DB 217 -----DS-----IHQDYTQGLIRMAVAGVLEVALDAL 245
QY 289 AEDWHSRRKRLRHGRVAVCRP 308
DB 246 VENNHSHTALNKEASADVAEP 266

RESULT 5
killer cell inhibitory receptor p91A precursor - mouse
JC5894
C:Species: Mus musculus (house mouse)
C:Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 17-Mar-1999
C:Accession: J05894
R:Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.; Ohya
J. Biochem. 123, 358-368, 1998
A:Title: Genomic structures and chromosomal location of p91, a novel murine regulatory
A:Reference number: J05894; MUID:98218758; PMID:9538215
A:Accession: J05894
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-841 <YAM>
A:Cross-references: GB:AF040946
C:Comment: This protein function as inhibitory cell-surface molecule against cell activ
C:Genetics:
A:Map position: 7
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-841/Product: Killer cell inhibitory receptor p91A #status predicted <YAT>
F:24-118,119-220,221-315,316-418,419-517,518-618/Domain: extracellular Ig-like #status p
F:618-674/Domain: transmembrane #status predicted <TM>
F:675-765/Domain: cytoplasmic #status predicted <CYT>

Query Match 20.5% Score 372.5; Db 2; Length 841;
Best Local Similarity 38.5% Pred: No. 2,26-19;
Matches 60; Conservative 35; Mismatches 76; Indels 17; Gaps 3;

QY 22 SGPFLKPSLQALPSSLVPLEKFTYLRCCGPGVGLYRLKSSSRVQDAV----- 73
DB 220 SGTLQKPTKAEKRGSVITSKRAMTIWCCGNLDAEVYFLHNESGCKTQSTCTCCGPNKGR 279
QY 74 FIPAYKRSLSAGPYRCQSYQNGSLMSLPSDQLEHVAATGVFA--KPSLSAGPGPAVSSGGGV 130
DB 280 FIPSWTRQHASQYRCYCYGASAGSPSDTLELVTCYEHVYKRLSLPSPVYTAGGNM 339
QY 131 TFGCCTRYGFDGFALYKED-----PAPYKPERWYRASFP--ITVTAAHSGTYRCYCSFS 184
DB 340 TLHCASDFHYCKFLTKEDKKFGNSLLEHSSSSQRYRALFICPTTPTHTGTRCYCYF 399
QY 185 SROPYLMASAPSDPELVYTGTSVTPSR 212
DB 400 KNAPQLMSVPSDQLQCLISGLSKKPSLL 427

RESULT 6
killer cell inhibitory receptor p91C precursor - mouse
JC5896
C:Species: Mus musculus (house mouse)
C:Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 05-Nov-1999
C:Accession: J05896
R:Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.; Ohya
J. Biochem. 123, 358-368, 1998
A:Title: Genomic structures and chromosomal location of p91, a novel murine regulatory
A:Reference number: J05894; MUID:98218758; PMID:9538215
A:Accession: J05896

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[illegible]

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RESULT 7
G02630
EcalphaRb - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
C/Accession: G02630
R/van Dijk, T.E.; Morton, H.C.; Caldenhoven, E.; Bracke, W.; Raaijmakers, J.A.M.; Ja
submitted to the EMBL Data Library, April 1996
A/Reference number: H01508
A/Accession: G02630
A/Status: preliminary; translated from GS/EXBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-239 <VAN>
A/Cross-references: EMBL:U56236; NID:g1326226; PTD:g1326229

Query Match
Best Local Similarity 20.1%; Score 358.5; DB 2; Length 239;
Matches 84; Conservative 35; Mismatches 95; Inlets 13; Gaps 3;

Cy 1 MSRSFTALFCLSLCLG-RVFAOSGLFLPKPSLQALPDSLVPLEKPTVLRQCSPPGVDLYEL 59
Dh 1 MDPKQITLCLVPLCLGORLQAQSGDPPMPFISAKSSVIFLDGSKVKLQCCAIRAVYITQL 60
Cy 60 EKUSSRYQD-----QAVLFFPAMKRLAGRYRCSYQNGSLMSLPSDQLELVAT 108
Dh 61 MINKSTYREIGRKLKFWNETDPPEVLDHMDANKAGRYQCQYRIGHYRFRYSCTLELVAT 120
Cy 109 GVFAKPSLSAQPGPAVSSGGDVTLLQCQTRY-GFDQFALYKSGDPAPYKNPERKWPASFP 167
Dh 121 GLYKGFPLSADRGVLMPEGENISLTCSAHIPFDRESLAKEGEGLSLPQHSGEHPANFSJ 180
Cy 168 ITVTAHSGYRCYSSFSRRDPYLMASPSDPLELVATG 204
Dh 181 GFDVLNVSGLYRCYGVNRSPLYLWSPSNALVELVATG 217

RESULT 8
JC5895
Killer cell inhibitory receptor p918 precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 05-Nov-1999
C/Accession: JC5895
R/Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.;
J. Biochem. 123, 358-368, 1998

```

A/Title: Genomic structures and chromosomal location of p91, a novel murine regulatory
A/Reference number: J05894; MIMD:38218758; PMID:9538215
A/Accession: J05895
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-680 <YAM>
A/Cross-references: GB:A7041035; MID:g2791691; PIDN:AAB36927.1; PID:g2791692
C/Comment: This protein function as inhibitory cell-surface molecule against cell activa
C/Genetics:
A/Map position: 7
F.1-23/Domain: signal sequence #status predicted <SIG>
F.24-118,119-220,221-315,316-418,419-517,518-618/Domain: extracellular Ig-like #status p
F.636-674/Domain: transmembrane #status predicted <TM>
F.675-680/Domain: cytoplasmic #status predicted <CYT>

Query Match 20.0%; Score 356.5; DB 2; Length 680;
Best local Similarity 22.9%; Pred. No. 2.5e-18;
Matches 106; Conservative 50; Mismatches 111; Indels 135; Gaps 7;

QY 22 SGPFLPKPSLQALPSSSLVPLEKPVTLRCQPPGVCLYRLEKSSSRVQCAVL----- 73
DB 220 SGNLQKPTTKAEPGSVITGKAMTIWCGNLDAAEVFLHNEKSKTOSTQTLCQPKNGR 279
QY 74 -FIPAMKPSLAGRYPCSYONSLSLSPDLELVATGVFA--KPSLSAQPAPAVSSGSDV 130
DB 280 EFIPSVTQAHGQYRCYCYSSAAGMSQPSLLELVATGVTEYNEPRLSLPSVTRPGSM 319
QY 131 TLCCQTRKCFDQFALYKEG-----PAPYKXPERKWRASPIITVTAASGTYRCYSF 184
DB 340 TLHCASQGHYCKFILTKEDKAFANALDTEHISSSRQYQALFIQPTPTHGTFRGYGV 399
QY 185 SRCPYLSAPSDPLELVATGVTPS----- 210
DB 400 KNPQQLMSVPSNLQQLISLSLSKPSLTLHGCHLDPGMTTLQCFSDMYDRAFLKYG 459
QY 211 -----R 211
DB 460 GADTWCHSSQQLDIFSVANFTLVVSSSTGGQYRCYGAHLSSKMSASEFLDILITGQ 519
QY 212 LPTEPPSSV-----AE 222
DB 520 LPTEPSLSVQNHVTHSGETVSLCMSMDSVTFILSKESGAQCPLRLKSKSHDQSSQAE 579
QY 223 FS-----EATAELTVSPNKVFTTEHSRSITTSFKES 254
DB 580 FMSAVTSHLSGTYRCYGAQSSSYLLSSASAPVELIVS-----GTIESSSKPFRP 631
QY 255 DSPAGPARQYTKGNLVRIICGAVITILAGFLAEQWHSRK 296
DB 632 NPPIPTENCHEINLIRMGVAVVFIVLSIATEAKRSRRQ 673

RESULT 9
G31925
KIR (c1-11) NK receptor precursor protein - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C/Accession: G01925; I61726
R/Magatman, N.
submitted to the EMBL Data Library, June 1995
A/Reference number: G08782
A/Accession: G01925
A/Status: preliminary; translated from GB/EMBL/DDJ
A/Molecule type: mRNA
A/Residues: 1-444 <WAG>
A/Cross-references: EMBL:U30274; NID:g1004360; PIDN:AAB52522.1; PID:g1004361
R/Columbia, M.; Samaridis, J.
Science 266, 405-408, 1995
A/Title: Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-B
A/Reference number: A56247; MIMD:95232526; PMID:7715543
A/Accession: I61726
A/Status: preliminary; translated from GB/EMBL/DDJ
A/Molecule type: mRNA

A/Residues: 1-444 <RES>
A/Cross-references: GB:U41269; NID:g780307; PIDN:AAA69870.1; PID:g780308
C/Genetics:
A/Gene: NKAT-3
A/Map position: 19

Query Match 18.8%; Score 335; DB 2; Length 444;
Best local Similarity 30.4%; Pred. No. 5.6e-17;
Matches 112; Conservative 34; Mismatches 127; Indels 96; Gaps 12;

QY 1 WSPPTALFCIDLCGRVP-----ACSGD-----FKPSIQALPSSVPLEKPV 45
DB 82 WSPVTAHAGNYTCRSHPSPTGWSAPSPVYIMVTGNHKKPSLAAHGPVXSGERY 141
QY 46 LRCQPPGVCLYRLEKISSRYCQDAV-----LFPAKMSLAGRYC----- 88
DB 142 LQWSDIMFEHFFLHKEGISKDFSRJWGQHDSVSKANPS-GPMLALAGTYRCYSVT 201
QY 89 -SYQMSLWSLPDQLFLVATGVFAKPSLSAQPAPAVSSGSDVTLCCQTRYGHDQFALYK 147
DB 202 TPYQ---LSAFSDPLDIVTGPYEKPSLSAQFGPKVQAGEVTLSCSSRSSYDMYHSR 257
QY 148 EGPAPRYKNP-----ERNVPSPIITVTAASGTYRCYSSSRDPYKASASDPLELV 202
DB 258 EGAHERLPAVRKVRNRFQALFPL--GPAHGGTYRCGSGFRHSPEYKSDPSDPLVSV 315
QY 203 TGTSVTPSRLPTEPPSSVAESEAATAELTVSPNKVFTTEHSRITTSFKESDSPAQPAR 262
DB 316 TG-----NPSSS-----WSPTESSSKSGNPR 337
QY 263 QVYTKGNLVRIICGAVITILAGFLAEQWHSRRKRLRHGRVAVQRPFPDPELQTRKSH 322
DB 338 HJH---LIGTEVVIIDFILFELLHWGSKK-----NAAV-----MDGEPAQNRTA 383
QY 323 GQDQGRQD 331
DB 384 NSEDSDEQD 392

RESULT 10
B53434
cell surface glycoprotein gp49b form 2 precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 05-Nov-1999
C/Accession: B53434
R/Castells, M.C.; Wu, X.; Arm, J.P.; Auster, K.F.; Katz, H.R.
J. Biol. Chem. 269, 6393-6401, 1994
A/Title: Cloning of the gp49B gene of the immunoglobulin superfamily and demonstrat
A/Reference number: A53434; MIMD:94179223; PMID:8132564
A/Accession: B53434
A/Status: preliminary
A/Molecule type: DNA; mRNA
A/Residues: 1-296 <CAS>
A/Cross-references: GB:U05265; NID:g475446; PIDN:AAA17798.1; PID:g475448; GB:U05266;
C/Genetics:
A/Gene: gp49B
A/Introns: 12/3; 24/2; 119/2; 220/1; 232/1; 249/3; 272/1
C/Keywords: alternative splicing; glycoprotein

Query Match 18.5%; Score 330; DB 2; Length 296;
Best local Similarity 36.1%; Pred. No. 7.9e-17;
Matches 88; Conservative 33; Mismatches 101; Indels 22; Gaps 6;

QY 6 TALFCJGLCL-GRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVCLYRLEKLS 64
DB 6 TVLLYLGLILBPRCAVQAGHLPRPIIWAEPGSVTAAYTSVITWCGSWEAQYVHLKES 65
QY 65 SRVQD-----CAVLFIPAMKPSLAGRYPCSYONSLSLSPDLELVATGVFAKPS 115
DB 66 VNPMDTQVPLETRKAKFNIPSTTSYAGTYKCYVESAGFSHSDAYELVMGAYENPS 125
QY 116 LSAQPPAPVSSGSDVTLCCQTRYGFDQFALYKEG-----DAPYKXPERKWRASPI 167
DB 116 LSAQPPAPVSSGSDVTLCCQTRYGFDQFALYKEG-----DAPYKXPERKWRASPI 167

```

DB      126  LSVYPSNVTSGVSISSFCSSSTVFGRFLLIQEKGKSLSTLDSQHQANQPSY--AATVVL 153
QY      158  ITVIAHSGTYRCYSPSSSDPYLMSAPSPLELVVTGTSVTPSRLPTEPSSVAEF-SEA 226
DB      154  DAVTPNENGTFRCYGFRRNEPQVMSKPSLDMXISSTK-DQSTPTIEDASVKNTQSEN 242
QY      227  TAEI 230
DB      243  NAEI 246

```

RESULT 11

A56247

natural killer cell-associated protein - human

C/Species: Homo sapiens (man)

C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999

C/Accession: A56247

R/Colonna, M.; Samaridis, J.

Science 268, 405-408, 1995

A/Title: Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-B

A/Reference number: A56247; MCID:95232526; PMID:7716543

A/Accession: A56247

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-348 <RES>

A/Cross-references: GB:L41267; NID:G780303; P/DN:AAA69868.1; P/D:G780304

C/Genetics:

A/Gene: GDB:NKAT1

A/Cross-references: GDB:698165

A/Map position: 19

Query Match

Best local similarity 18.4%; Score 328; DB 2; Length 348;

Matches 101; Conservativity 34; Mismatches 107; Indels 64; Gaps 11;

```

QY      1  MSPSPALFGLGCT--GRVPAQSGPLPKPSLQALPESLVPLEKPYTLRQCGPFGVDLYR 58
DB      1  XSLVWSVACVGFLLQGAMP-HEGVHRKPSLLAHPGPLVKSEETVILQCSVDVRFQHL 59
QY      59  LEKLSSRYQD-----CAVLFIPAMKPSIAGRYRC-----SYQNGSLWSL 98
DB      60  LHR--EGMFNDLLELGEHHQGVSKANPSISMTQDIAGTYRCYGVTHSEFYQ---VSA 113
QY      99  PSDQLSVATGVFAKPSLSAQSPNAVSSGGDVTJCCQTRYGFDQFALYKSGDPAPYKRP 157
DB      114  PSDPLDVIIGLYEKPSLSAQSPFTVLAGEVNTLSCSSSSSYDMYHLSRGEAEHRRLPA 173
QY      158  ---ERWYRASFPILITVTAASGTYRCYSPSSRDPLYMSAPDPLELVVTGTSVTPSRLP 213
DB      174  GKXNGTFQADPPL--GPATHGTYRCFGSPHSPYKSKSGDFLLNSVTGKPSNSWSP 231
QY      214  TEPSSVAEFSEATAELTVSFTNKVFTTETSRISITSPKESDPSKGPAPGYVTKGTWR 273
DB      232  TEPSSK-----TGNNR-----LHI 246
QY      274  CLG---AVILITAGFLAEHMSRRK 296
DB      247  LIGTSVITLFIILFFLLHRCNSKK 272

```

RESULT 12

G01924

KIR (c1-2) NK receptor precursor - human

N/Alternate names: killer cell inhibitory receptor

C/Species: Homo sapiens (man)

C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999

C/Accession: G01924; G01945

R/Wagtmann, K.

submitted to the EMBL Data Library, June 1995

A/Reference number: G08780

A/Accession: G01924

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

```

A/Residues: 1-444 <WAG>
A/Cross-references: EMBL:J30273; NID:G1004358; P/DN:AA85252.1; P/D:G1004359
R/D/Andrea, A.; Chang, C.; Franz-Bacon, K.; McClean, T.; Phillips, C.H.; Janier,
submitted to the EMBL Data Library, July 1995
A/Reference number: G08908
A/Accession: G01945
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-444 <DXA>
A/Cross-references: EMBL:U31416; NID:G973405; P/DN:AA023725.1; P/D:G973406
C/Genetics:
A/Gene: NKX1

```

Query Match

Best local similarity 18.3%; Score 327; DB 2; Length 444;

Matches 111; Conservativity 34; Mismatches 128; Indels 96; Gaps 12;

```

QY      1  MSPSPALFGLGCTGRVP-----AQGDP-----PKSLQATPSSLVPLEKPYT 45
DB      52  MSPVTTAHAGNYTCRGSHPSPTGWSAPSNPVYIVYTGTHRKPSSLAHPGPLVKSGERVI 141
QY      46  LRQCGPFGVDLYRLEKLSSRYQDQAV-----LTPYAKRSLAGRYRC----- 88
DB      42  LQWSDIMFEHFHLKRGISKDPISRLVQGIHDGVSKANPS-CPMMLALAGTYRCYGSVTH 201
QY      89  -SYQNGSLWS-SSDQELVATGVFAKPSLSAQSPNAVSSGGDVTJCCQTRYGFDQFALYK 147
DB      202  TPYQ---LSAPSDPLDIVTGYEKPSLSAQPGPKVQAGEVTLSCSSRSSYDMYHLSR 257
QY      148  ESDPAPYKNP-----ERWYRASFPILITVTAASGTYRCYSPSSRDPLYMSAPDPLELV 202
DB      258  ERGAHERLLPAVRKVRRTFQADPPL--GPATHGTYRCFGSPHSPYKSKSGDFLLNSV 315
QY      203  TGTSTVTPSRLPTEPSSVAEFSEATAELTVSFTNKVFTTETSRISITSPKESDPSAPAR 262
DB      316  TG-----NFS-------WPSPTFPSSKSGMPR 337
QY      263  QVYTKGNLVRICGAVILITAGFLAEHMSRRKRLRHRGAVQRPPLPFPQTRKSH 322
DB      338  HLHI---LIGTSVITLFIILFFLLHRCNSKK-----NAAV-----MDQEPAGNRTA 383
QY      323  GCGDGGRCQ 331
DB      384  NSBDSDQCD 392

```

RESULT 13

I61725

natural killer cell associated transcript 2 - human

C/Species: Homo sapiens (man)

C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Nov-1999

C/Accession: I61725

R/Colonna, M.; Samaridis, J.

Science 268, 405-408, 1995

A/Title: Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-B

A/Reference number: A56247; MUID:95232526; PMID:7716543

A/Accession: I61725

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-341 <RES>

A/Cross-references: GB:L41268; NID:G780305; P/DN:AAA69869.1; P/D:G780306

C/Genetics:

A/Gene: NKAT-2

Query Match

Best local similarity 18.1%; Score 323.5; DB 2; Length 341;

Matches 99; Conservativity 36; Mismatches 105; Indels 89; Gaps 12;

```

QY      1  MSPSPALFGLGCT--GRVPAQSGPLPKPSLQALPSSLVPLEKPYTLRQCGPFGVDLYR 58
DB      1  XSLVWSVACVGFLLQGAMP-HEGVHRKPSLLAHPGPLVKSEETVILQCSVDVRFQHL 59
QY      59  LEKLSSRYQD-----CAVLFIPAMKPSIAGRYRC-----SYQNGSLWSL 98

```

```

DB 60 LHR--EGKFRDTHLIGEHHDGVSKANFSIGPMKQDLAAGTYRCYGSVTHSPYQ-----LSA 113
QY 99 PSQQLVATGVFAKPSLSAQPGPAVSSGGEDVTJQCQTRYGFDQFALYKEG-----P 151
DB 114 PSQPLDIVITGLYEKPSLSAQPGPTVLAGESVTLSCSSSSSYDMYHLSREGEAHERESA 173
QY 152 APYKPERMYRASFPITITVAHSGTYRCYSSSRDPYKMSAPSEPLELVITGTSVTSR 211
DB 174 GPXWNGT--FOADFP--GEATHGGTYRCGSPRDSFYKMSNSDPLLVSVTGNPSKSWP 229
QY 212 LPTSPSSVAEFSSEATAEITVSTNKFVTTETSRSTTSRKESDSPAGARQYVTKGNY 271
DB 230 SPTSPSS-----TGNPRH-----L 244
QY 272 RICLGA---VILITLAGTAECDWHSRRX 296
DB 245 HVLIGTSVAILPILLFLLFLLHRCCKKX 273

```

```

RESULT 14
T09402
Immunoglobulin-like protein IGSP1 - human
C/Species: Homo sapiens (man)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jun-2000
C/Accession: T09402
R/Mazzarella, R.; Pengue, G.; Jones, J.; Jones, C.; Schlossinger, D.
Genomics 48, 157-162, 1998
A/Title: Cloning and expression of an immunoglobulin superfamily gene (IGSP1) in Xq25.
A/Reference number: Z16655; MIM:38190514; PMID:9521868
A/Accession: T09402
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1327 <MAZ>
A/Cross-references: EMBL:AF034198; NID:g2645889; PDB:AAO52057.1; PID:g26458890
C/Genetics:
A/Gene: IGSP1
A/Map position: Xq25

```

```

Query Match 18.0%; Score 322; DB 2; Length 1327;
Best Local Similarity 32.1%; Pred. No. 18-15;
Matches 105; Conservative 37; Mismatches 133; Indels 52; Gaps 9;

```

```

QY 26 PKPSJQALPSGLVPLEKPVITRCQGP--PGVDLYRLEKSSSRV---QDQAVLPIPAY 75
DB 960 PKPWLFAPSSSVPMQNVTLNCRGSPVHGVYILHKEGATSYQLKSGTSTNDGAFPTNT 1019
QY 79 KSLLAGRYRCSYQ--NSGLWLPSCDLELVATGVFAKPSLSAQPGPAVSSGGDVTJQCQ 135
DB 1020 SGTSMGRYSCCHPDWTSSIKIQPSKTELELVTLGPKPSLSAQPGPAVAGENMTJQCQ 1079
QY 136 TRYGFDFALYKEG--DPAFYKPERMYRASFPITITVAHSGTYRCYSSSRDPYKMSA 193
DB 1080 GELPDSTFVLKKEGAQEPJQGRPS--GYRADFWYPAVGEQSGYSCVYIDSTPRASN 1138
QY 194 PSQPLELVITGTSVTS-----RLPTSPSSVAEF-----SEATAEIT- 231
DB 1139 HSDSLRHWTDKPKPSLSAESTMFKLGKDTIQCRGSLPGVEFVLEHDEGAPOQSE 1198
QY 232 -----VSFTKVFTESTRSITTSFKSSCSAPARQYVTKGNYRITL 275
DB 1199 DGLFVINNVEGKIGNYSCSYRLCAYPDIMSPSDPLELVGAGAPVAQECTVGNVRSST 1258
QY 276 GAVILITLAGFLADWHSRRXLRHG 302
DB 1259 LVVVVVALGVLAIEW-KKWRRLRTG 1284

```

```

RESULT 15
A53434
cell surface glycoprotein gp49b form 1 precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 05-Nov-1999

```

```

C/Accession: A53434
R/Castells, M.C.; Wu, X.; Arm, J.P.; Auster, K.F.; Katz, H.R.
J. Biol. Chem. 269, 8393-8401, 1994
A/Title: Cloning of the gp49b gene of the immunoglobulin superfamily and demonstration
A/Reference number: A53434; MIM:194179223; PMID:8132564
A/Accession: A53434
A/Status: preliminary
A/Molecule type: DNA; mRNA
A/Residues: 1-335 <CAS>
A/Cross-references: GB:U05265; NID:g475446; PDB:AAA17797.1; PID:g475447; GB:U05264;
C/Genetics:
A/Gene: gp49B
A/Intons: 12/3; 24/2; 119/2; 220/1; 232/2; 271/2; 288/3; 311/2
C/Keywords: alternative splicing; glycoprotein

```

```

Query Match 17.8%; Score 317.5; DB 2; Length 335;
Best Local Similarity 34.0%; Pred. No. 7.5e-16;
Matches 84; Conservative 36; Mismatches 104; Indels 23; Gaps 6;
QY 6 TATFCLGLCL-GRVPAQSGPLPKPSLQACPSLVPLEKPYTLRCQGPFGVDLYRLEKLS 64
DB 6 TVLYLGLLEPRITAVQAGHLPKPIIWAEPGSVIAAYTSVITKCGSWEAQYHLYKXS 65
QY 65 SRVOD-----QAVLFFAMKRLAGRYRCSYONGSLMSLPSDQLELVATGVFAKPS 115
DB 66 VNPWDQVPLETRNKAKFNFSMTTSYAGTYKCYESAAGPSEHSDAMELVYTGAYENPS 125
QY 116 LSNQGPVAVSSGGDVTJQCQTRRYGFDQFALYKEG-----DPAFYKPERMYRASFP 167
DB 126 LSVYSSSNVTSQVSISSSCSSIVFGRFILQEGKGLSWTLDSQHCAQDSY--ATFV 183
QY 168 TVTAAHSGTYRCYSSSRDPYKMSAPSEPLELVITGTSVTSRRLTEPTSPSSVAEFSSEAT 227
DB 184 DAVTPNHNGTFRCYGYFRNEPQVMSKPSNSLDNISSTK--DGLETYQKIL 240
QY 228 AELTVSF 234
DB 241 LGVLVSF 247

```

```

Search completed: October 23, 2003, 09:43:01
Job time : 45 secs

```


GenScan version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

CM protein - protein search, using sw model

Run on: October 23, 2003, 09:38:24 ; Search time 23 Seconds

(without alignments)
693.133 Million cell updates/sec

Title: US-09-503-387-3

Perfect score: 1786

Sequence: 1 MSPSPALFCLGLCGRYPA.....KSHGCGDGRQDVHSGJCS 339

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	392	21.9	287	FCAR_HUMAN	P24071 homo sapien
2	342.5	19.2	367	K3S1_HUMAN	Q14343 homo sapien
3	340	19.0	377	K204_HUMAN	Q99706 homo sapien
4	335	18.9	444	K3L1_HUMAN	P43629 h killer ce
5	330.5	18.5	304	K2S2_HUMAN	P43631 homo sapien
6	329	18.4	348	K2L2_HUMAN	P43627 homo sapien
7	328	18.4	348	K2L1_HUMAN	P43626 h killer ce
8	325.5	18.2	304	K2S1_HUMAN	Q14954 homo sapien
9	320.5	18.1	341	K2L3_HUMAN	P43628 h killer ce
10	320.5	17.9	304	K2S4_HUMAN	P43632 homo sapien
11	319	17.9	455	K3L2_HUMAN	P43630 homo sapien
12	317.5	17.8	335	G49B_MOUSE	Q64261 mus musculu
13	307	17.2	304	K2S5_HUMAN	Q14953 homo sapien
14	299	16.7	304	K2S3_HUMAN	Q14952 homo sapien
15	289.5	16.2	303	G49A_MOUSE	Q61450 mus musculu
16	143.5	9.3	485	A1BQ_HUMAN	P64217 homo sapien
17	136	7.6	291	DN43_DIDYR	P82957 didelphis m
18	126.5	7.1	3707	PGBX_MOUSE	Q65793 mus musculu
19	123.5	6.9	267	FCG3_RAT	P27645 rattus norv
20	118	6.6	4391	PGBX_HUMAN	P98160 homo sapien
21	116	6.5	2774	MAPA_RAT	P34926 rattus norv
22	115.5	6.5	1709	SN_HUMAN	Q98222 homo sapien
23	113.5	6.4	1284	NRCA_CHICK	P35331 gallus gall
24	108	6.3	257	FCGA_HUMAN	P13119 homo sapien
25	108	6.3	341	FCG2_CAVPO	Q60513 cavia porce
26	107	6.3	261	FCG3_MOUSE	P08508 mus musculu
27	106.5	6.0	3375	UN52_CAEEL	Q06561 caenorabdi
28	106	5.9	285	FCG2_RAT	Q63203 rattus norv
29	106	5.9	739	VCA1_MOUSE	P29533 mus musculu
30	106	5.9	2161	SHK1_HUMAN	O91566 homo sapien
31	105.5	5.9	330	FCG2_MOUSE	P38101 mus musculu
32	104	5.8	447	AYBN_HUMAN	Q96706 homo sapien
33	104	5.8	740	PEC1_PIG	Q95242 sus scrofa

34	104	5.8	1367	1	AMYH_YEAST	P08640 saccharomyc
35	103.5	5.8	770	1	DAB2_HUMAN	P98092 homo sapien
36	102.5	5.7	912	1	ICAS_RABIT	Q29730 oryctolagus
37	101.5	5.7	727	1	PEC1_MOUSE	Q08481 mus musculu
38	101	5.7	296	1	FCG2_BOVIN	Q28110 bos taurus
39	101	5.7	404	1	FCG1_MOUSE	P26151 mus musculu
40	101	5.7	3149	1	TEGU_EBV	P01156 epstein-bar
41	100.5	5.6	1051	1	PTK7_CHICK	Q91048 gallus gall
42	100	5.6	739	1	VCA1_RAT	P29534 rattus norv
43	99.5	5.6	1887	1	RPB1_DROME	P04052 drosophila
44	99	5.5	404	1	RAGE_HUMAN	Q15109 homo sapien
45	99	5.5	739	1	VCA1_HUMAN	P13320 homo sapien

ALIGNMENTS

RESULT 1
FCAR_HUMAN STANDARD; PRT; 287 AA.
AC P24071; Q13603; Q13604; Q15727; Q15728; Q92590;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Immunoglobulin alpha Fc receptor precursor (IgA Fc receptor; (CD89
antigen).
GN FCAR OR CD89.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homin;
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A.1).
RX MEDLINE=91079769; PubMed=2258698;
RA Maliszewski C.R., March C.J., Schoenborn M.A., Gimpel S., Shen J.;
RT "Expression cloning of a human Fc receptor for IgA";
RL J. Exp. Med. 172:1665-1672(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM A.1).
RC TISSUE=Bone marrow;
RX MEDLINE=95363085; PubMed=7636189;
RA de Wit T.P.M., Morton H.C., Capel P.C.A., van de Winkel J.G.J.;
RT "Structure of the gene for the human myeloid IgA Fc receptor (CD89).";
RL J. Immunol. 155:1203-1209(1995).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS A.2 AND A.3).
RC TISSUE=Alveolar macrophage, and Monocytes;
RX MEDLINE=56247667; PubMed=866619;
RA Parry C., Sibille Y., Lehen A., Monteiro R.C.;
RT "Identification of Fc alpha receptor (CD89) isoforms generated by
alternative splicing that are differentially expressed between blood
monocytes and alveolar macrophages";
RL J. Immunol. 156:4442-4448(1996).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS B AND B-DELTA-S2).
RA van Dick T.B., Morton H.C., Gaidehenoven E., Bracke M.,
RA Raaijmakers J.A.M., Lamers J.W.C., Koenderman B., Groot R.P.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBFJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM A.3).
RX MEDLINE=96433090; PubMed=8836118;
RA Pleass R.C., Andrews P.D., Kerr M.A., Woof C.M.;
RT "Alternative splicing of the human IgA Fc receptor CD89 in
neutrophils and eosinophils";
RL Biochem. J. 318:771-777(1996).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM J02).
RA Toyabe S., Kuwano Y., Takeda K., Uchiyama Y., Abo T.;
RT "Alternatively spliced forms of monocyte IgA Fc receptors in patients
with IgA nephropathy";
RJ Submitted (SEP-1996) to the EMBL/GenBank/DBFJ databases.
RN [7]
RP SUBUNITS.

```

RX MEDLINE=84375887; PubMed=7522255;
RA Pfeifferhorn L.C., Yeaman G.R.;
RT "Association of IgA-Fc receptors (Fc alpha R) with Fc epsilon RI
RT gamma 2 subunits in U937 cells. Aggregation induces the tyrosine
RT phosphorylation of gamma 2."
RT J. Immunol. 153:3228-3236(1994).
CC -1- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS ALPHA.
CC MEDIATES SEVERAL FUNCTIONS INCLUDING CYTOKINE PRODUCTION.
CC -1- SUBJECT: ASSOCIATES WITH THE FC EPSILON RI GAMMA 2 RECEPTOR
CC INDUCING TYROSINE PHOSPHORYLATION OF GAMMA 2.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (FORM A) AND SOLUBLE
CC (FORM B).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=6;
CC Comment=Additional isoforms seem to exist;
CC Name=A.1;
CC IsoId=P24071-1; Sequence=Displayed;
CC Name=A.2;
CC IsoId=P24071-2; Sequence=VSP_002635;
CC Name=A.3; Synonyms=RIA2;
CC IsoId=P24071-3; Sequence=VSP_002634;
CC Name=B;
CC IsoId=P24071-4; Sequence=VSP_002636;
CC Name=B delta-S2;
CC IsoId=P24071-5; Sequence=VSP_002632, VSP_002636;
CC Name=U02;
CC IsoId=P24071-6; Sequence=VSP_002633, VSP_002635;
CC -1- TISSUE SPECIFICITY: DIFFERENTIALLY EXPRESSED BETWEEN BLOOD AND
CC MUCOSAL MYELOID CELLS. MONOCYTES EXPRESS ISOFORMS A.1, A.2 AND A.3
CC WHILE ALVEOLAR MACROPHAGES EXPRESS A.1 AND A.2 TRANSCRIPTS;
CC HOWEVER THEY EXPRESS ONLY ONE ISOFORM AT THEIR SURFACES.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 2 immunoglobulin-like C2-type domains.
CC -1- DATABASE: NAME=PROCM; NOTE=CCD guide C089 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cc/cds.htm".
CC
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CC
DR EMBL; X54150; CAA38089.1; -
DR EMBL; X87767; CAA61039.1; -
DR EMBL; X87768; CAA61039.1; JOINED.
DR EMBL; X87769; CAA61039.1; JOINED.
DR EMBL; X87766; CAA61039.1; JOINED.
DR EMBL; X87765; CAA61039.1; JOINED.
DR EMBL; U43774; AAC50639.1; -
DR EMBL; U43677; AAC50595.1; -
DR EMBL; U56236; AAB00566.1; -
DR EMBL; U56237; AAB00567.1; -
DR EMBL; S82919; AAD14421.1; -
DR EMBL; D87859; BAA13477.1; -
DR F1R; G02630; G02630.
DR F1R; JH0332; JH0332.
DR HSSP; P43626; INKR.
DR Genew; H3NC13608; FCAR.
DR X1M; 147345; -
DR GO; GO:0005887; C:Integral to plasma membrane; TAS.
DR GO; GO:0006955; P:Immune response; TAS.
DR InterPro; IPR003593; I9.
DR InterPro; IPR003006; I9_MHC.
DR Pfam; PF00347; I9_2.
DR SMART; SMC0409; I9_2.
DR PROSITE; PS50835; I9_LIKE; FALSE NEG.
KM Receptor; Glycoprotein; Transmembrane; IgA-binding protein;
KM Immunoglobulin domain; Repeat; Signal; Alternative splicing.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 287 IMMUNOGLOBULIN ALPHA FC RECEPTOR.
FT DOMAIN 22 227 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 228 246 POTENTIAL.
FT DOMAIN 247 287 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 107 IG-LIKE C2-TYPE 1.
FT DOMAIN 139 220 IG-LIKE C2-TYPE 2.
FT DISULFID 49 100 BY SIMILARITY.
FT DISULFID 146 193 BY SIMILARITY.
FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPPLIC 12 23 Missing (in isoform B-delta-S2).
FT VARSPPLIC 24 24 /FTId=VSP_002632.
FT VARSPPLIC 24 24 G -> GRV:SEHFWCRSLGCPNVNDAAGRFG (in
FT VARSPPLIC 24 24 isoform U02).
FT VARSPPLIC 121 216 /FTId=VSP_002633.
FT VARSPPLIC 195 216 Missing (in isoform A.3).
FT VARSPPLIC 195 216 /FTId=VSP_002634.
FT VARSPPLIC 217 267 Missing (in isoform A.2 and isoform U02).
FT VARSPPLIC 217 267 /FTId=VSP_002635.
FT VARSPPLIC 217 267 DSIHQDTTQNIIRMAVAGLVLVALALVENWHSHTALNK
FT VARSPPLIC 217 267 PASADVAEDPSWQCMQDGLTFAITPSVCK -> GRV:PVQ
FT VARSPPLIC 217 267 PCVWVGCPGPGHRAGI (in isoform B and
FT VARSPPLIC 217 267 isoform B-delta-S2).
FT VARSPPLIC 217 267 /FTId=VSP_002636.
FT SEQUENCE 287 AA; 3226 MW; A2CCA68467CD45F7 CRC64;
SQ
Query Match 21.9%; Score 392; DE 1; Length 287;
Best Local Similarity 31.2%; Pred. No. 4,7e-22;
Matches 100; Conservative 43; Mismatches 110; Indels 68; Gaps 5;
CY : MSRSPTALFCICICIG-RVPAOSGFLPKPSLQALPSSILVPLEKPVTLRCGPPGVGYR. 59
EB 1 MDPKQTLGLVLCIGRIQAGGDFPMPFISAKSSVYPLDGSVKICQQAIREAVLTQ. 60
CY 60 EKLSRSRYQD-----QAVLFIPANKPSLAGRYRSYONGSLWSPSDQFLVAT 108
EB 61 KIKNSTYREGRJUKFWNEPTDEPVIDHNDANKAGRYCCYRIGHYREYSDTLELVVT 120
CY 109 GVEAKPSLSAQGPVAVSSGGVTLQCGTRY-GEDCFALYKFGDPAPYKPRFWRKASFI 167
EB 121 GLYGKPLSAGRLVLMNGENISLTSSAHIPDRFSLAKGELSLPQSGEHFANFSL 180
CY 168 ITVTAHSGTRCYGSSFRDPYLSAPSDLELVVTGTSVTPSPRLPTSPSSVAEFSRAT 227
EB 181 GPVLDLWSGTRCYGWNRPYLSFSPKALELVVT----- 216
CY 228 AELTVSFTNKVFTETISRS-TTSPKESDSPAGPARQYTKGNLVRICGAVILLIAGFI 267
EB 217 -----DS-----IHQDYTCMLIRMAVAGLVALALIL 245
CY 268 AEDWHSRRKRLRHGRAVQRP 308
EB 246 VENWHSHTALNKEASADVAPR 266
RESULT 2
K3S1_HUMAN
ID K3S1_HUMAN STANDARD; PRT; 387 AA.
AC Q14943;
DT 01-NOV-1997 (Rel. 35, Created)
ET 01-NOV-1997 (Rel. 35, Last sequence update)
ET 15-SEP-2003 (Rel. 42, Last annotation update)
FE Killer cell immunoglobulin-like receptor 3DS1 precursor (MHC class I
DE NK cell receptor) (Natural killer associated transcript 10) (NKAT-10).
GN KIR3DS1 OR NKAT10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=96270004; PubMed=8662091;
RA Boehring C., Samaridis J., Colonna M.;
RT "Alternatively spliced forms of human killer inhibitory receptors."
RL Immunogenetics 44:227-230(1996).
RN [2].
RP VARIANT HIS-166.
RX MEDLINE=98090086; PubMed=9430221;
RA Ueberberg M., Valiante N.M., Shum B.P., Shilling H.G.,
RA Liener-Waldenbach K., Corliss B., Tyan D., Lanier L.J., Parham P.;
RT "Human diversity in killer cell inhibitory receptor genes."
RL Immunity 7:753-763(1997).
CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
CC DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
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CC -----
DR EMBL: L76661; AAB36589.1; .
DR HSSP: P43626; INKR.
DR Genew: HGNC:6340; KIR3DSL.
DR MIM: 604957; .
DR GO: GO:0005897; C:intracel. to plasma membrane; NAS.
DR GO: GO:0003793; F:defense/immunity protein activity; NAS.
DR GO: GO:0030106; F:MHC class I receptor activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR GO: GO:0030101; P:natural killer cell activation; NAS.
DR InterPro: IPR003599; Iq.
DR InterPro: IPR003006; Iq_MHC.
DR Pfam: PF00347; Iq; 3.
DR SMART: SM00409; Iq; 3.
DR PROSITE: PSS0835; IG_LIKE; FALSE_NEG.
KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW Repeat; Multigene family; Polymorphism.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 367 KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
FT 306.
FT DOMAIN 22 340 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 341 360 POTENTIAL.
FT DOMAIN 361 387 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 102 IG-LIKE C2-TYPE 1.
FT DOMAIN 137 202 IG-LIKE C2-TYPE 2.
FT DOMAIN 237 300 IG-LIKE C2-TYPE 3.
FT DISULFID 49 95 BY SIMILARITY.
FT DISULFID 144 195 BY SIMILARITY.
FT DISULFID 244 283 BY SIMILARITY.
FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 166 R->H.
SC SEQUENCE 387 AA; 42902 MW; 0375CE73DD155100 CRC64;
Query Match 19.2%; Score 342.5; DN 1; Length 367;
Best Local Similarity 35.8%; Pred. No. 3e-18;
Matches 101; Conservative 27; Mismatches 105; Indels 43; Gaps 9;
CY 1 MSPSPALFGLGICLRVP-----AGSGP-----FKPSICAPSSLVLEKAVT 45
DB 82 MSPVTTAHAGNYTCRGSHPHSEGTGMSAPSNMWIVTGNHRKPSLAPGPLVKSGERVI 141
CY 46 LRQGGPVGVDLYRUEK-----LSSRYQDQ-----AVLFPAKMSLAGRYRC----- 58
DB 142 LQKMSDIMEHFELHKEMISKPSRLVGQHDGVSKANFSIGSMRALAGTYRCYSVTH 201
CY 89 -SYNGSLWSPSDQLVLWAGVFAKPSLSAOPGPAVSSGDDVTLCQCTRYGDFQFALYK 147

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DB 202 TFYQ-----USAPSDPLDIWVTGLYKESLSAQPGPKQAQGESVT;SCSSRSSYDNYHLNR 257
CY 148 EGDPAFYKVP-----ERWYRASFPITVTAAHSGTYECYSSSSRDYPLWSAPSDP;FLWV 202
DB 258 EGAHERRLPAVRKVNRTFQADFL--GPATHGCTVRCFGSFRHSDYEMSDPSDPLVSV 315
CY 203 TGTSVTPRLPLTEFPSSVAEFSE-----ATAELTSGFTNKVP 225
DB 316 TGNPSSWSWSPTEPSSKGNLRHLHLIGTSVVKIPRTLLF 357
RESULTS 3
K2L4_HUMAN
ID K2L4_HUMAN STANDARD; PRT; 377 AA.
AC Q99706; O14621; O14622; O14623; O14624; C43534; P78400; P78401;
AC Q99559; Q99560; Q99561; Q99562; Q99077;
DT 16-OCT-2001 (Rel. 40, Created)
DT 15-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Killer cell immunoglobulin-like receptor 2DL4 precursor (MHC class I
DE NK cell receptor KIR103AS) (Killer cell inhibitory receptor 103AS)
DE (KIR-103AS) (G9P).
GN KIR2DL4 OR KIR103AS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1].
RP SEQUENCE FROM N.A.
RX MEDLINE=97102173; PubMed=9946692;
RA Selvakumar A., Steffens U., Dupont B.;
RT "NK cell receptor gene of the KIR family with two IG domains but
RL highest homology to KIR receptors with three IG domains."
RL Tissue Antigens 48:285-294(1996).
RN [2].
RP SEQUENCE FROM N.A. (ISOFORMS 1; 3; 4 AND 5).
RX MEDLINE=9737880; PubMed=9234477;
RA Selvakumar A., Steffens U., Palanisamy N., Chaganti R.S.K., Dupont B.;
RT "Genomic organization and allelic polymorphism of the human killer
RL cell inhibitory receptor gene KIR103."
RL Tissue Antigens 49:564-573(1997).
RN [3].
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 6).
RC TISSUE=Lymphoid;
RA Biasoni R.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4].
RP SEQUENCE FROM N.A., AND VARIANTS.
RX MEDLINE=98090086; PubMed=9430221;
RA Ueberberg M., Valiante N.M., Shum B.P., Shilling H.G.,
RA Liener-Waldenbach K., Corliss B., Tyan D., Lanier L.J., Parham P.;
RT "Human diversity in killer cell inhibitory receptor genes."
RL Immunity 7:753-763(1997).
RN [5].
RP SEQUENCE FROM N.A.
RA Chan H.W., Salter R.D.;
RT "Exon deletion contributes to structural diversity of 2DL4 killer
RT inhibitory receptors."
RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [6].
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=97213129; PubMed=9059894;
RA Selvakumar A.;
RT "Polymorphism and domain variability of human killer cell inhibitory
RL receptors."
RL Immunol. Rev. 155:183-196(1997).
CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
CC -1- INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING CELL LYSIS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=6;
CC Name=1;

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RT and HLA-B recognition by human natural killer cells.";
RL Science 268:405-408(1995).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood lymphocytes;
RX MEDLINE=96111967; PubMed=8777725;
RA Wagtmann N., Rajagopalan S., Winter C.C., Peruzzi M., Jong E.C.,
RT "Killer cell inhibitory receptors specific for HLA-C and HLA-B
RL identified by direct binding and by functional transfer.";
RN Immunity 3:801-809(1995).
RN (3)
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood lymphocytes;
RX MEDLINE=96343861; PubMed=8760804;
RA Pende D., Biassoni R., Cantoni C., Verdiani S., Falco M.,
RT "The natural killer cell receptor specific for HLA-A allotypes: a
RT novel member of the p58/p70 family of inhibitory receptors that is
RT characterized by three immunoglobulin-like domains and is expressed
RT as a 140-kD disulphide-linked dimer.";
RL J. Exp. Med. 184:505-518(1996).
RN (4)
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95378652; PubMed=7650366;
RA D'Andrea A., Chang C., Franz-Bacon K., McClanahan T., Phillips C.H.,
RT "Molecular cloning of NKBI, A natural killer cell receptor for HLA-B
RT allotypes.";
RL J. Immunol. 155:2306-2310(1995).
RN (5)
RP SEQUENCE FROM N.A. AND VARIANTS.
RX MEDLINE=98090086; PubMed=9430221;
RA Urbriegs M., Vallante N.M., Shum B.F., Shilling H.G.,
RA Lienert-Weidenbach K., Corliss B., Ryan D., Lanier L.L., Parham P.,
RT "Human diversity in killer cell inhibitory receptor genes.";
RL Immunity 7:753-763(1997).
CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA BW4
CC ALLELE. INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING
CC CELL LYSIS.
CC -1- SUBCELLULAR LOCATION: Type I Membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: L41269; AAA69870.1; -
DR EMBL: J33273; AAB52521.1; -
DR EMBL: J33274; AAB52522.1; -
DR EMBL: X94262; CAA63938.1; -
DR EMBL: J31416; AAC23725.1; -
DR EMBL: AF022049; AAB95322.1; -
DR PIR: G01925; G01925.
DR HSSP: P43625; INKR.
DR Genew: HGNC:6338; KIR3DL1.
DR MIM: 604946; -
DR GO: GO:0005887; C:integral to plasma membrane; NAS.
DR GO: GO:0003793; F:defense/immunity protein activity; NAS.
DR GO: GO:0030109; F:HLA-B specific inhibitory MHC class I recep. . .; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR GO: GO:0030102; P:negative regulation of natural killer cell . . .; NAS.
DR InterPro: IPR003593; IG.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; IG_3.
DR SMART: SM00409; IG_3.
DR PROSITE: PS50835; IG_LIKE; FALSE_NEG.
KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;

KW Repeat; Multigene family; Polymorphism.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 444 KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
FT
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FT DOVAIN 22 340 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 341 360 POTENTIAL.
FT DOVAIN 361 444 CYTOPLASMIC (POTENTIAL).
FT DOVAIN 42 102 IG-LIKE C2-TYPE 1.
FT DOVAIN 137 202 IG-LIKE C2-TYPE 2.
FT DOVAIN 237 300 IG-LIKE C2-TYPE 3.
FT DISULFID 49 95 BY SIMILARITY.
FT DISULFID 144 195 BY SIMILARITY.
FT DISULFID 244 293 BY SIMILARITY.
FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 2 2 S -> L.
FT VARIANT 13 13 /FTID=VAR_010319.
FT VARIANT 23 23 L -> F.
FT VARIANT 23 23 /FTID=VAR_010320.
FT VARIANT 23 23 M -> V.
FT VARIANT 68 68 /FTID=VAR_010321.
FT VARIANT 68 68 - -> V.
FT VARIANT 75 75 /FTID=VAR_010322.
FT VARIANT 75 75 I -> L.
FT VARIANT 259 259 /FTID=VAR_010323.
FT VARIANT 259 259 G -> R.
FT VARIANT 333 333 /FTID=VAR_010336.
FT VARIANT 333 333 S -> C.
FT SEQUENCE 444 AA; 49098 MW; 47DEA12BBAFDEC53 CRC64;
SQ
Query Match 38.8%; Score 335; DB 1; length 444;
Best Local Similarity 30.4%; Pred. No. 13e-17;
Matches 112; Conservative 34; Mismatches 127; Indels 96; Gaps 12;
CY 1 MSPSPFALFCLGICLGRV-----AQSGL-----PKSLQALPSIVPEKPV 45
D0 92 MSPVTAHAGNYTCRGSHPHSPGTSAPSAPSNPVIMVTGNARKPSJLHPGFVXGGERV 141
CY 45 LRQGPVVDLYRDEKLSRSYQDAV-----LFLPMKRSIAGRYRC----- 88
D0 142 LQWSDIMFEHFLHKEGISKPSRLVGQIHGVSKANPSIGFMMLALAGTYRCYSVTH 201
CY 89 -SIQNGSLMSPSQJELVATGYFAKPSLSAQGPVAVSSGGVTLCCQTRYGDFALYK 147
D0 202 TPIQ---LSAPSDPLDVTVTGYEKPSLSAQGPVQAGSEVTLSCSSRSRYDMYHJSR 257
CY 148 EGDPAFYKP-----ERWRASPPITVTAAHSGTYRCYSSSRDPYJWSAPDFLELV 202
D0 253 EGGAEHRRJPAVRKVRNRTQADPPL--GPAIHGCTYRCPSGRHSPYEKSDPSDPLVSV 315
CY 203 TGTSVTPSRJPTPEPSSVAAPSELTALVTFINKVFTTETSISITTSPEKSDSPAGPAR 262
D0 316 TG-----NDSSS-----WSPTEPSSKSGNR 317
CY 263 QYTKGNLYRICGAVITLILASFLAEDWHSRRKRLRHPRGAVQRPJPPPLFQTRKSH 322
D0 338 HLHT---LIGTSVITLIFLLFLHJMSCKK-----NAAV-----MDGEPAGNRTA 383
CY 323 GGGDGGRCQ 331
D0 384 NSEDSDEQD 392
RESULT 5
K2S2_HUMAN STANDARD; PRT; 304 AA.
AC P43631; Q14955;
DT 01-NOV-1995 (Rel. 32, Created)
DT 16-OCT-2001 (Rel. 40, last sequence update)
DT 15-SEP-2003 (Rel. 42, last annotation update)
DE Killer cell immunoglobulin-like receptor 2DS2 precursor (MHC class I

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LE NK cell receptor) (Natural killer associated transcript 5) (NKAT-5)
DE (p58 natural killer cell receptor clone Cl-49) (p58 NK receptor) (NK
DE receptor 183 Act1).
GN KIR2DS2 OR NKAT5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE OF 2-334 FROM N.A.
RC TISSUE=Natural killer cells;
PX MEDLINE=95269128; PubMed=7749980;
RA Wagtmann N., Biassoni R., Cantoni C., Verdiani S., Mainati M.S.,
RA Vitale M., Bottino C., Moretta L., Moretta A., Long E.O.;
RT "Molecular clones of the p58 NK cell receptor reveal immunoglobulin-
RT related molecules with diversity in both the extra- and intracellular
RT domains."
RJ Immunity 2:439-449(1995).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=95232526; PubMed=7716543;
RA Colonna M., Samaridis J.;
RT "Cloning of immunoglobulin-superfamily members associated with HLA-C
RT and HLA-B recognition by human natural killer cells."
RJ Science 268:405-408(1995).
RN (3)
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RX MEDLINE=96195217; PubMed=8627776;
RA Biassoni R., Cantoni C., Falco M., Verdiani S., Bottino C., Vitale M.,
RA Conte R., Possi A., Moretta A., Moretta L.;
RT "The human leukocyte antigen (HLA)-C-specific 'activatory' or
RT 'inhibitory' natural killer cell receptors display highly homologous
RT extracellular domains but differ in their transmembrane and
RT intracytoplasmic portions."
RJ Exp. Med. 183:645-650(1996).
RN (4)
RP FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
CC DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC
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CC
DR EMBL: U24079; AAC50338.1; ALT_INIT.
DR EMBL: U41347; AAA65225.1; .
DR EMBL: X89693; CAA61983.1; .
DR HSSP: P43626; INKR.
DR Genew: HGNC:6334; KIR2DS2.
DR MIM: 604953; .
DR GO: GO:0016021; C:integral to membrane; NAS.
DR GO: GO:0004888; F:transmembrane receptor activity; NAS.
DR GO: GO:0006955; F:immune response; NAS.
DR InterPro: IPR003599; IG.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; IG_2.
DR SMART: SM00409; IG_1.
DR PROSITE: PS50835; IG_LIKE; FALSE_NEG.
KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW Repeat; Multigene family.
FT CHAIN 1 21 BY SIMILARITY.
FT CHAIN 22 304 KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
FT 2052.
FT UGMAN 22 245 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 246 265 POTENTIAL.
FT DOMAIN 266 304 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 107 IG-LIKE C2-TYPE 1.

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FT DOMAIN 142 205 IG-LIKE C2-TYPE 2.
FT DISULFID 49 100 BY SIMILARITY.
FT DISULFID 149 198 BY SIMILARITY.
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 20 20 W -> G (IN REF. 3).
SQ SEQUENCE 304 AA; 33501 MW; 186C77DD9E86BA28 CRC64;

Query Match 18.5%; Score 330.5; DB 1; Length 304;
Best Local Similarity 33.1%; Pred. No. 1.7e-17;
Matches 101; Conservative 35; Mismatches 105; Indels 61; Gaps 12;

QY 1 MSPSPALFCLGLCL--GRVPAQSGPLPKPSLOALPSSJVFLEKPVTRCCGPPGVDR 59
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1 MSIMVSMACVGFPL..QGAWP-HEGVHRKPSLLAHPGPVKSSETVILQCMGVAREHFL 59
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

QY 59 LEKSSSRVQD-----QAVLFIPAKRSLASGRRC-----SYQNSIMSL 98
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 60 LHR--EGKYKDTLHLIGEHHDGYSKANFSIGPMQDLAQTVCYSVTHSRVQ---LSA 113
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

QY 99 FSDQELVATGVFAKPSLSAQCPGPAVSSGGCVTLCCQTRYGFDQALYKEGD-----F 151
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 114 FSDQDLIVITGLYEKPSLSAQCPGPAVLAGSVTLSCSRSSQDMVHLISREGAFHFRFSA 173
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

QY 152 AFYKNEPERVYRASFPTITVTAHSGTYRCYSPSSRCQPYLMSAPDPLELVITGVTPSR 211
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 174 GFKNQGT--FGADPPL--GPATNGCTYRCFSGFRCSFYENSSDPLVSVTGKPSNSWP 229
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

QY 212 LPRPPSSVAFFSE-----ATAEITVSFT-----NK-----VPTTSSRSITTS 250
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 233 SPTEPSSSKTGNPRHLHLVIGTSVVKIPFTLLFLHHRWCSKNKAAMVDPAQNRIVN 289
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

QY 251 PKESD 255
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 290 SEDSD 294

RESULT 6
K2L2_HUMAN STANDARD; PRT; 348 AA.
ID K2L2_HUMAN
AC P43627; Q14951;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Killer cell immunoglobulin-like receptor 2DL2 precursor (MHC class I
DE NK cell receptor) (Natural killer associated transcript 6) (NKAT 6)
DE (p58 natural killer cell receptor clone Cl-43) (p58 NK receptor).
GN KIR2D2 OR NKAT6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Natural killer cells;
RX MEDLINE=95269128; PubMed=7749980;
RA Wagtmann N., Biassoni R., Cantoni C., Verdiani S., Mainati M.S.,
RA Vitale M., Bottino C., Moretta L., Moretta A., Long E.O.;
RT "Molecular clones of the p58 NK cell receptor reveal immunoglobulin-
RT related molecules with diversity in both the extra- and intracellular
RT domains."
RJ Immunity 2:439-449(1995).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=96270004; PubMed=8662091;
RA Dohring C., Samaridis J., Colonna M.;
RT "Alternatively spliced forms of human killer killer inhibitory receptors."
RJ Immunogenetics 44:227-230(1996).
RN (3)
RP FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C
RN ALLELES. INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING
RN CELL LYSIS.
CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein.

```

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CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -----
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CC -----
DR EMBL: U24075; AAC50334.1; -
DR EMBL: U24075; AAC50334.1; -
DR PDB: 1EFX; 14-CON-00.
DR PDB: 2DL2; 29-DEC-99.
DR PDB: 2DL1; 05-MAY-03.
DR Genem: HGNC:6330; KIR2DL2.
DR MIM: 604937; -
DR InterPro: IPR003599; I9.
DR InterPro: IPR003599; I9.
DR Pfam: PF00347; I9; 2.
DR SMART: SM00409; I9; 1.
DR PROSITE: PS00835; IG_LIKE; FALSE NEG.
DR Receptor: Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
DR Repeat: Multigene family; 3D-structure.
DR SIGNAL: 21 BY SIMILARITY.
DR CHAIN: 22 348 KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
DR 2DL2.
DR DOMAIN: 22 245 EXTRACELLULAR (POTENTIAL).
DR TRANSMEM: 246 264 POTENTIAL.
DR DOMAIN: 265 348 CYTOPLASMIC (POTENTIAL).
DR DOMAIN: 42 107 IG-LIKE C2-TYPE 1.
DR DOMAIN: 142 205 IG-LIKE C2-TYPE 2.
DR DISTUFID: 49 100 BY SIMILARITY.
DR DISTUFID: 149 198 BY SIMILARITY.
DR CARBOHYD: 84 84 N-LINKED (GICNAC. . .) (POTENTIAL).
DR CARBOHYD: 178 178 N-LINKED (GICNAC. . .) (POTENTIAL).
DR CARBOHYD: 211 211 N-LINKED (GICNAC. . .) (POTENTIAL).
DR CONFLICT: 289 SF -> RQ (IN REF. 2).
DR SEQUENCE: 348 AA; 38472 MW; 5B54C548F5CF3FBF CRC64;

Query Match 18.4%; Score 329; DB 1; Length 348;
Best Local Similarity 31.1%; Pred. No. 2.6e-17;
Matches 102; Conservative 34; Mismatches 104; Indels 85; Gaps 12;

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AC P43626; Q43470;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Killer cell immunoglobulin-like receptor 2DL1 precursor (MHC class I
DE NK cell receptor) (Natural killer cell associated transcript 1) (NKAT-1)
DE (p58 natural killer cell receptor clones CL-42/47.11) (p58 NK
DE receptor) (p58.1 MHC class-I specific NK receptor).
GN KIR2DL1 OR NKAT1 OR CD158A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Natural killer cells;
RX MEDLINE=95232526; PubMed=7716543;
RA Colonna M., Samaridis J.;
RT "Cloning of immunoglobulin-superfamily members associated with HLA-C
RT and HLA-B recognition by human natural killer cells.";
RL Science 268:405-408(1995).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 22-45.
RC TISSUE=Natural killer cells;
RX MEDLINE=95269128; PubMed=7749980;
RA Wagtmann N., Biassoni R., Cantoni C., Verdiani S., Malnati M.S.,
RA Vitale M., Bottino C., Moretta L., Moretta A., Long E.O.;
RT "Molecular clones of the p58 NK cell receptor reveal immunoglobulin-
RT related molecules with diversity in both the extra- and intracellular
RT domains.";
RL Immunity 2:439-449(1995).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS.
RX MEDLINE=96090086; PubMed=9430221;
RA Unberg V., Valiante N.M., Shum B.P., Shilling H.G.,
RA Liener-Weidenbach K., Corliss B., Ryan D., Lanier L.L., Parham P.;
RT "Human diversity in killer cell inhibitory receptor genes.";
RL Immunity 7:753-763(1997).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 27-221.
RX MEDLINE=97433335; PubMed=9288975;
RA Fan Q.R., Mosyak J., Winter C.C., Wagtmann N., Long E.O., Wiley D.C.;
RT "Structure of the inhibitory receptor for human natural killer cells
RT resembles haematopoietic receptors.";
RL Nature 389:95-100(1997).
CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
CC INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING CELL LYSIS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U24075; AAC50335.1; -
DR EMBL: U24075; AAC50335.1; -
DR EMBL: U24075; AAC50337.1; -
DR EMBL: AF022045; AAB95318.1; -
DR PIR: A56247; A56247.
DR PIR: A56247; A56247.
DR PDB: 1MX3; 11-NOV-98.
DR PDB: 1MX3; 30-MAY-01.
DR Genem: HGNC:6329; KIR2DL1.
DR MIM: 604936; -
DR GO: GO:0005887; C: integral to plasma membrane; TAS.
DR GO: GO:0004872; F: receptor activity; TAS.
DR GO: GO:0006955; P: immune response; TAS.
DR InterPro: IPR003599; I9.
DR InterPro: IPR003006; IG_MHC.

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DR PFAM: PF00047; Ig; 2.
DR SMART: SMO0409; IG; 1.
DR PROSITE: PSS0835; IG_LIKE; FALSE_NEG.
KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
FT Repeat; Multigene family; Polymorphism; 3D-structure.
FT SIGNAL 21
FT CHAIN 22 348
FT
FT DOMAIN 22 245
FT TRANSMEM 246 264
FT DOMAIN 265 348
FT DOMAIN 42 107
FT DOMAIN 142 205
FT DISULFID 49 100
FT DISULFID 149 198
FT CARBOHYD 67 67
FT CARBOHYD 84 84
FT CARBOHYD 144 144
FT CARBOHYD 178 178
FT VARIANT 5 5
FT VARIANT 37 37
FT VARIANT 135 135
FT VARIANT 175 175
FT VARIANT 184 184
FT VARIANT 203 203
FT VARIANT 237 237
FT VARIANT 266 266
FT STRAND 30 34
FT STRAND 38 40
FT TURN 41 42
FT STRAND 45 51
FT STRAND 57 63
FT STRAND 65 73
FT STRAND 75 77
FT TURN 78 79
FT STRAND 80 87
FT HELIX 92 94
FT STRAND 96 104
FT TURN 105 106
FT STRAND 107 107
FT TURN 108 109
FT STRAND 118 123
FT STRAND 130 134
FT STRAND 138 139
FT TURN 141 142
FT STRAND 144 151
FT STRAND 157 162
FT TURN 163 164
FT STRAND 169 172
FT STRAND 174 177
FT TURN 179 179
FT STRAND 180 185
FT STRAND 194 202
FT TURN 203 204
FT STRAND 205 209
FT STRAND 216 223
SQ SEQUENCE 348 AA; 38504 MW; 3DFBF2D6FDCED1D1E CRC64;
Query Match 18.4%; Score 325; EB 1; Length 348;
Best Local Similarity 31.0%; Freq. No. 3.1e-17;
Matches 101; Conservative 34; Mismatches 107; Indels 84; Gaps 11;
CY 1 NSPSPALFGLGLG--GRVPAQSGPDPKPSJQALPSSLVPTLEKPVTLKCGSPFGVTLK 58
DB 1.MSLIVVSWACVGFLLQGAKP-HEGVHRRKPSLLAFPSPLVKSFEETVLQCSDMFEPHF 59

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CY 59 LEKSSSRVOD-----QAVLIPAKKSLAGRYRC-----SYNGSLWSJ 98
DB 60 LHR-EGMENDTLRLIGEHHDGVSKNFSISRMQDLAGTRYCGSVTHSPYQ---VSA 113
CY 99 PSDQLELVATGVFAKPSLSAQPSVAVSSGGVTLQCQTRYGPDQFALYKEGDPAPYKP- 157
DB 114 PSDPLDIYIIGLYEKPSLSAQPGPTVLAGEVTLSCSSRSSYDYVHLSREGAEHRRLLPA 173
CY 159 ---ERWYRASPIITVTAHSGTYRCYSPSSRDPLYKMSAPSDPELVLTGTSVTPSRP 213
DB 174 GPKVNGTQACDPL--GPAHGGTYRCFGSPHDSPEYKSKSDPLVSVTGNPNSWPSF 231
CY 214 TEPPSVAEFSEATAEVTSFTNKVTTETSRSLTSPKESDSQAPARQYTKNLVRI 273
DB 232 TEPSK-----TGNPRH-----LHI 246
CY 274 CUG--AVLITLAGFAEDWHSRK 296
DB 247 LIGTSVTLIFLFLFLHKKCSNKK 272
RESULT 8
K2S1 HUMAN STANDARD; PRT; 304 AA.
AC Q14954; Q43471;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Killer cell immunoglobulin-like receptor 2DS1 precursor (MHC class I
DE NK cell receptor Eb6 Act1).
GN KIR2DS1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
RN 1.
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RX MEDLINE=96195217; PubMed=8627176;
RA Siasson R., Cantoni C., Falco M., Verdiani S., Bottino C., Vitale M.,
RA Conte R., Poggi A., Moretta A., Moretta L.;
RT "The human leukocyte antigen (HLA)-C-specific 'activatory' or
RT 'inhibitory' natural killer cell receptors display highly homologous
RT extracellular domains but differ in their transmembrane and
RT intracytoplasmic portions.";
RJ J. Exp. Med. 183:645-653 (1995).
EN 121
SEQUENCE FROM N.A. AND VARIANT LYS-91.
RX MEDLINE=98093086; PubMed=9433221;
RA Uthberg M., Valianze N.M., Stum B.P., Shilling H.G.,
RA Liener-Wedenbach K., Colliss B., Ryan D., Lanier L.J., Parham P.;
RT "Human diversity in killer cell inhibitory receptor genes.";
RL Immunity 7:753-763 (1997).
CC -!- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLIELES.
CC DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: X09892; CAA61982.1;
DR EMBL: AF022046; AAB95319.1;
DR HSSP: P43626; 1NKR.
DR Genew: HGNC:6333; KIR2DS1.
DR MIM: 604952; -.

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Query Match	18.24	Score 325.5	33.1	Length 304
Best Local Similarity	33.98	Prod. No. 4.1e-17		
Matches 92	Conservative 35	Mismatches 103	Indels 41	Gaps 9

RESULT

RX MEDLINE=95232526; PubMed=77165433

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RA Colonna M., Samaridis C.;
RT "Cloning of immunoglobulin-superfamily members associated with HLA-C
RT and HLA-B recognition by human natural killer cells.";
RL Science 268:405-408(1995).
RN 21
RP SEQUENCE FROM N.A.
RC TISSUE=Natural killer cells;
RX MEDLINE=95269128; PubMed=7749980;
RA Wagtmann N., Blassanti R., Cantoni C., Verdiani S., Mainati M.S.,
RA Vitale V., Bottino C., Moretta L., Moretta A., Long E.O.;
RT "Molecular clones of the p58 NK cell receptor reveal immunoglobulin-
RT related molecules with diversity in both the extra- and intracellular
RT domains.";
RL Immunity 2:439-449(1995).
RN 31
RP SEQUENCE FROM N.A., AND VARIANTS AAA-9; ARG-32; GGU-56; ARG-71 AND
RP HIS-318.
RX MEDLINE=96090086; PubMed=9430221;
RA Ueberberg M., Valliante N.M., Shum B.P., Shilling H.G.,
RA Lienert-Wiedebach K., Corliss B., Tyen D., Lantier L.L., Parham P.;
RT "Human diversity in killer cell inhibitory receptor genes.";
RL Immunity 7:753-763(1997).
CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
CC INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING CELL LYSIS.
CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -----
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CC -----
DR EMBL: L41268; AAA69869.1; -
DR EMBL: U24074; AAC50333.1; -
DR EMBL: AF022048; AAB95321.1; -
DR PIR: I61725; I61725.
DR HSSP: P43626; INKR.
DR Genew: HGNC:6331; KIR2DL3.
DR MIM: 604938; -
DR GO: GO:0016021; C:integral to membrane; TAS.
DR GO: GO:0004872; F:receptor activity; TAS.
DR GO: GO:0006955; P:immune response; TAS.
DR InterPro: IPR003599; 19.
DR InterPro: IPR003006; 19_MHC.
DR Pfam: PF00047; 19_2.
DR SMART: SW00409; 19_1.
DR PROSITE: PS50835; 19_LIKE; FALSE_NEG.
KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW Repeat; Multigene family; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 341
FT FT 22 341
FT FT 22 341
FT DOXAIN 22 245
FT TRANSMEM 246 265
FT DOXAIN 266 341
FT DOXAIN 42 137
FT DOXAIN 42 205
FT DISULFID 49 133
FT DISULFID 149 198
FT CARBOHYD 84 84
FT CARBOHYD 178 178
FT CARBOHYD 211 211
FT VARIANT 9 9
FT VARIANT 32 32
FT VARIANT 56 56
FT VARIANT 71 71
FT VARIANT 71 71
H -> R

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FT FT VARIANT 318 318 /FTID=VAR_010316.
FT FT SEQUENCE 341 AA: 37886 XM: C21EAF80EA9AAB2 CRO664; R -> H. /FTID=VAR_010317.
SQ SEQUENCE 341 AA: 37886 XM: C21EAF80EA9AAB2 CRO664; R -> H. /FTID=VAR_010317.

Query Match 18.1%; Score 323.5; EB 1; Length 341;
Best Local Similarity 30.1%; Pred. No. 6,6e-17;
Matches 95; Conservative 36; Mismatches 105; Indels 89; Gaps 12

QY 1 MSPSPALFCLGCL--GRVPAQSGFLPKPSICALPSSIVPLEKPTLRQCGPFGVDIYR 53
DB 1 MSLMVAWVQVGFLLQGWMP-HGVYRKPSILAHQGLVXSEFTVILQGWSDVRFQHD 59
QY 59 LEKSSGRYOD-----CAVLFPAMKRSLAGRYRC-----SYQNSIMSI 98
DB 60 LHR--EGRFKDILHIGEHHDGVSARKNESIGPMNQLAGIYRQYGVTHSPYQ---ISA 113
QY 99 PSCQLSLVATGVFAKPSISAOQPDVAVSSGGVTDCCQTRVGFQDFALYKGD-----P 151
DB 114 PSDPLDIIVITGLYKPSLSAQPGFVLAGESTVLSGSSRSSTDMYHLRSGEAMHERKSA 173
QY 152 APYKPEERWYRASFFITVTAAGSTYRCVSSSRDPFHWASPDPLSLVTVTSVPSR 211
DB 174 GPKVNGT--FQADPFL--GPAHGGTYRCFSGSRDPSREKNSGSDPLVSVTGNSKSWF 229
QY 212 LPTSPSSVAEPSEATAELTVAFTKRVFTTETSSITSPSSGSDPAQPARQYTKGVLY 271
DB 230 SPTSPSE-----TONPRH----- 284
QY 272 RICLSA---VLTTLGFLAEQWHSRK 296
DB 245 NVLIGTSVITLIFLLIFLLHRCCKRK 273

RESULT 10
K2S4 HUMAN STANDARD; PRI: 304 AA.
ID K2S4 HUMAN STANDARD; PRI: 304 AA.
AC P43612;
DT 01-NOV-1995 (Rel. 32, Created);
DT 01-NOV-1997 (Rel. 35, Last sequence update);
DT 15-SEP-2003 (Rel. 42, Last annotation update);
DE Killer cell immunoglobulin-like receptor 2S4 precursor (XHC class -
DE NK cell receptor) (Natural killer killer associated transcript 8) (NKAT-8)
DE (P58 natural killer cell receptor clone CL-39) (P58 NK receptor) (CL-
DE 17).
CN KIR2DS4 OR NKAT8 OR KKA3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID:9606;
CX 11;
RN 11;
RP SEQUENCE FROM N.A.
RC TISSUE=Natural killer cells;
RX MEDLINE=95269128; PubMed=7749990;
RA Wagtmann N., Blassoni R., Cantoni C., Verdiani S., Mainati M.S.,
RA Vitale M., Bottino C., Moretta L., Moretta A., Jong E.C.;
RA "Molecular clones of the p58 NK cell receptor reveal immunoglobulin-
RA related molecules with diversity in both the extra- and intracellular
RA domains.";
RT Immunity 2:439-449(1995);
RN 12;
RP SEQUENCE FROM N.A.
RX MEDLINE=96270004; PubMed=8662091;
RA Doehring C., Samaridis U., Colonna M.;
RA "Alternatively spliced forms of human killer inhibitory receptors";
RL Immunogenetics 44:127-230(1996);
RN 13;
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RX MEDLINE=96350503; PubMed=8765026;
RA Bottino C., Sivori S., Vitale M., Cantoni C., Falco M., Pende D.,
RA Moretta L., Augugliaro R., Semenzato G., Blassoni R., Moretta L.,
RA Moretta A.;

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RT      "A novel surface molecule homologous to the p58/p50 family of
RT      receptors is selectively expressed on a subset of human natural
RT      killer cells and induces both triggering of cell functions and
RT      proliferation."
RT      Eur. J. Immunol. 26:1816-1824 (1996).
RN      [4].
RP      SEQUENCE FROM N.A.
RA      Chan H.W., Salter R.D.
RL      Submitted (May-1997) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
CC      DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC      -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC
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CC      or send an email to license@isb-sib.ch).
CC
CC      -----
CC      EMBL: U24077; AAC50336.1; AJ2_1117.
CC      EMBL: L76671; AAB36599.1; .
CC      EMBL: X54609; CAA64317.1; .
CC      EMBL: AF02235; AAB61281.1; .
CC      HSSP: P43626; INKR.
CC      Genew: HGNC:6336; KIR2DS4.
CC      MIM: 604955; .
CC      GO: GO:005887; C:integral to plasma membrane; TAS.
CC      GO: GO:003822; F:MHC-interacting protein; TAS.
CC      InterPro: IPR003599; 19.
CC      InterPro: IPR003006; 19_MHC.
CC      Pfam: PF00047; 19/2.
CC      SMART: SM00409; 19_1.
CC      PROSITE: PS50835; IG_LIKE, FALSE_NEG.
CC      KW      Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
CC      Repeat; Multigene family.
CC      FT      SIGNAL 1 21
CC      FT      CHAIN 22 304
CC
CC      FT      DOMAIN 22 245
CC      FT      TRANSMEM 246 265
CC      FT      DOMAIN 266 304
CC      FT      DOMAIN 42 107
CC      FT      DOMAIN 142 205
CC      FT      DISULFID 49 103
CC      FT      DISULFID 149 198
CC      FT      CARBOHYD 67 67
CC      FT      CARBOHYD 84 94
CC      FT      CARBOHYD 144 144
CC      FT      CARBOHYD 178 178
CC      FT      CARBOHYD 211 211
CC      FT      SEQUENCE 304 AA; 33583 MW; 33583 MW; CEFD4F3FED679A3F CRC64;
CC
CC      Query Match 17.9% Score 320.5; DE 1; Length 304;
CC      Best Local Similarity 35.9%; Pred. NO. 9.5e-17;
CC      Matches 97; Conservative 32; Mismatches 102; Indels 39; Gaps 11.
CC
CC      1 MSPSPALFGLG--GRAVAGSGPLPKPSQALPSSVLEKPVTLRQGGPGVD-- 55
CC      : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC      1 MSIMVIMACVGFPLGAMF-CEGVHRKPSFLALPGHIVKSEETVILQCSGVYEHFL 59
CC      : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC
CC      56 YRLEKLSSPY-----QDAVLFIPANKRSLAGRYP-----SYQNGSLMSLP 100
CC      : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC      60 LREGKFNNTLHIGEHSDGSKANFSIGMKPVLAGTYRCYGSVPHSPYQ----LSAPS 115
CC      : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC
CC      101 DQELVATGVAFAKPSLSAQDQPAVSSGGVLTLCQCTRYGFQFAVYKEGDPADYKNP-- 157
CC      : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC      116 DPEDMTVIGLEYEKPSLSAQDQPTVQAGENVTLSCSSRSSYDMYHLRSGZAEHRRLLPAVR 175
CC      : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC
CC      158 --ERWYRASPTITVTAAHSGTYRCYSSFSRC-PYLMASAPDPLEJVTGTSTPSRLPT 214

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Cc 176 SINGTQADFPD--CPATHCCTACGCG-SFRLAPYKNSNSDPLVSVTCGNSNSKSPPT 232
Cc 215 EPPSSVAEFSF-----ATAELTVSPKPKVP 213
Cc 233 EPPSSKTCGNPRHJHVLICTSVVKIPETILLF 262
Db 233 EPPSSKTCGNPRHJHVLICTSVVKIPETILLF 262

RESULT 1:
K3L2_HUMAN
ID K3L2_HUMAN STANDARD; FRT; 455 AA.
AC P43630; Q13238; Q14947; Q14948; Q32684; Q95367;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Killer cell immunoglobulin-like receptor 3DL2 precursor (MHC class I
DE NK cell receptor) (Natural killer killer associated transcript 4) (NKA7-4)
DE (p70 natural killer cell receptor clone CL-5).
GN KIR3DL2 OR NKAT4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Natural killer cells;
RX MEDLINE=95232526; PubMed=7716543;
RA Colonna M., Samaridis J.;
RT "Cloning of immunoglobulin-superfamily members associated with HLA-C
RT and HLA-B recognition by human natural killer cells.";
RL Science 268:405-408(1995).
RN 12
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood lymphocytes;
RX MEDLINE=9611967; PubMed=8777725;
RA Wagmann N., Rajagopalan S., Winter C.C., Petuzzi M., Jong E.C.;
RT "Killer cell inhibitory receptors specific for HLA-C and HLA-B
RT identified by direct binding and by functional transfer.";
RL Immunity 3:801-809(1995).
RN 13
RP SEQUENCE FROM N.A. AND VARIANT VAL-113.
RC TISSUE=Lymphoid;
RX MEDLINE=9634386; PubMed=6760804;
RA Pende D., Biassoni R., Cantoni C., Verdiani S., Falco M.,
RA di Donato C., Accame L., Bottino C., Moretta A., Moretta L.;
RT "The natural killer cell receptor specific for HLA-A allotypes: a
RT novel member of the p58/p70 family of inhibitory receptors that is
RT characterized by three immunoglobulin-like domains and is expressed as
RT a 140-kD disulphide-linked dimer.";
RL J. Exp. Med. 184:505-518(1996).
RN 14
RP SEQUENCE FROM N.A.
RX MEDLINE=96273004; PubMed=8662091;
RA Dohring C., Samaridis J., Colonna M.;
RT "Alternatively spliced forms of human killer inhibitory receptors.";
RL Immunogenetics 44:227-230(1996).
RN 15
RP VARIANTS ALA-40; VAL-113; ASP-158; HIS-166; PRO-228 AND THR-262.
RX MEDLINE=98090386; PubMed=9433221;
RA Unberg M., Valiante N.M., Shum B.P., Shilling H.G.,
RA Lierert-Weidenbach K., Collins B., Ryan D., Lanier L., Parham P.;
RT "Human diversity in killer cell inhibitory receptor genes.";
RL Immunity 7:753-763(1997).
Cc 1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-A ALLELES.
Cc 1- INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING CELL LYSIS.
Cc 1- SUBCELLULAR LOCATION: Type I transmembrane protein.
Cc 1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
Cc 1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
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Cc or send an email to license@ebi.ac.uk).
Cc -----
Cc DR EMBL: 541270; AAA69872.1; -
Cc DR EMBL: U30272; AAB52520.1; -
Cc DR EMBL: X93595; CAA63791.1; -
Cc DR EMBL: X94373; CAA64150.1; -
Cc DR EMBL: L76665; AAB36593.1; -
Cc DR EMBL: L76666; AAB36594.1; -
Cc DR HSSP: P43626; INKR.
Cc DR Genew; HGNC:6339; KIR3DL2.
Cc XTM: 604947; -.
Cc DR GO: 0005887; C: integral to plasma membrane; TAS.
Cc DR GO: 0003922; P: MHC-interacting protein; TAS.
Cc DR GO: 0006968; P: cellular defense response; TAS.
Cc DR InterPro: IPR003599; I9.
Cc DE InterPro: IPR003006; I9_MHC.
Cc DE Pfam: PF00347; I9_3.
Cc DR SMART; SMO0409; I9_2.
Cc DR PROSITE; PS00835; IG-LIKE, FALSE_NEG.
Cc XM Receptor; immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
Cc Repeat; Multigene family; Polymorphism.
Cc KM Repeat; Multigene family; Polymorphism.
Cc FT SIGNAL 1 21
Cc FT CHAIN 22 455
Cc FT 22 455
Cc FT DOMAIN 22 340
Cc FT TRANSMEM 341 360
Cc FT DOMAIN 361 455
Cc FT DOXAIN 42 102
Cc FT DOXAIN 137 202
Cc FT DOXAIN 237 300
Cc FT DISULFID 49 95
Cc FT DISULFID 144 195
Cc FT DISULFID 244 293
Cc FT CARBOHYD 179 179
Cc FT CARBOHYD 239 239
Cc FT CARBOHYD 273 273
Cc FT CARBOHYD 306 306
Cc FT VARIANT 40 40
Cc FT VARIANT 113 113
Cc FT VARIANT 158 158
Cc FT VARIANT 166 166
Cc FT VARIANT 228 228
Cc FT VARIANT 252 252
Cc FT VARIANT 252 252
Cc SC SEQUENCE 455 AA; 50230 MR; D34BA6B6B3C2945 CRC64;
Cc -----
Cc Query Match 17.9% Score 319; DB 1; Length 455;
Cc Best local similarity 30.7% Pred. No. 2e-16;
Cc Matches 105; Conservative 44; Mismatches 127; Indels 66; Gaps 15;
Cc -----
Cc QY 1 MSPSPALFCGLCL--GRVPAQSGPRLPRSLQALPSLSVLPKPYTLKCGGFGVLYR 58
Cc 1 MSLTVMACVGFLLJGAFELWGGQ-DKPLSLARPSVYPRGSHVALQCHYRGGFNEM 59
Cc 1 MSLTVMACVGFLLJGAFELWGGQ-DKPLSLARPSVYPRGSHVALQCHYRGGFNEM 59
Cc QY 59 LEXUSSR-----YCDQAVL--FLPMKRSLSARVCSYNGSL-----NSLPEDQ 102
Cc 60 LYKEDRSHVPIFRGRIFQESITMGVTPRAH---AGTYRC---RGRFHSITGWSAPSK 112
Cc 60 LYKEDRSHVPIFRGRIFQESITMGVTPRAH---AGTYRC---RGRFHSITGWSAPSK 112
Cc QY 103 LEVATGVFAKPSLSAQPRAVSSGGDYTLQOCRTYGFDPALYKESGPAFYKNPERWY 161
Cc 113 LVTMTGNHRKSLLAHPRLKSGETVLIDCWSVMFEFFLHREGIS---EDPSRQVG 169
Cc 113 LVTMTGNHRKSLLAHPRLKSGETVLIDCWSVMFEFFLHREGIS---EDPSRQVG 169
Cc QY 162 -----RASFLITVTAHSGTYRCYSSFRDFFYLWASPSDPLELVITGTSVTPSRLLPT 214
Cc 170 QHIDGVSKANISGLPLMFLVLAGTYRCYGVPHSPYGLSAPSDPLDIVITGLYKPS-LSA 226
Cc 170 QHIDGVSKANISGLPLMFLVLAGTYRCYGVPHSPYGLSAPSDPLDIVITGLYKPS-LSA 226

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CY 2.5 EPPSSVAHFESEAFALIVSFTNKVFTET-----SRITTSFK-----ESDSAGPARCY 264
DB 229 QPGFVQAGENVTLSCSSMSYDIYH--SRGEAHERRLRAVPRKVNRTFCADFLGPA--- 265
CY 265 YTKGNLVETCLGAV-----ILLIAGFLAEDWRS 293
DB 286 -THGIVR-CFGSFRA-PCWWSNSSDPLVSVTGNPSSSWPS 325

RESULT 12
G49B_MOUSE
ID G49B_MOUSE STANDARD; PRT; 335 AA.
AC Q64281; Q64312;
DT 01-NOV-1997 (Rel. 35, Created;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DS Mast cell surface glycoprotein GP49B precursor.
GN GP49B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
CY (1)
RP SEQUENCE FROM N.A. (ISOFORMS GP49B1 AND GP49B2).
RC STRAIN=C3H, and BALB/c; tissue=Bone marrow;
RX MEDLINE=9413923; PubMed=4132564;
RA Castellani M.C., Wu X., Alm J.P., Austen K.F., Katz H.R.;
RT "Cloning of the gp49b gene of the immunoglobulin superfamily and
RT cell surface protein originally described as gp49."
RT J. Biol. Chem. 269:8393-8402(1994).
RU (1)
CC -1- FUNCTION: MAY PLAY A ROLE IN CELL-CELL OR CELL-CYTOKINE
CC INTERACTIONS DURING THE DEVELOPMENT OF MAST CELLS FROM VULNERABLE
CC PROGENITORS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=GP49B1;
CC IsoId=Q64281-1; Sequence=Displayed;
CC Name=GP49B2;
CC IsoId=Q64312-2; Sequence=VSP_002510, VSP_002511;
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -1- This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL: J05266; AAA17799.1; -
DR EMBL: U05265; AAA17797.1; -
DR EMBL: J05265; AAA17798.1; -
DR EMBL: J05264; AAA17796.1; -
DR PIR: A53434; A53434.
DR PIR: B53434; B53434.
DR HSSP: P43626; INKR.
DR MGD: MGI:132701; Gp49b.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_2.
DR PROSITE: PS50835; IG_LIKE_1.
KW Signal; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
KW Alternative splicing.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 335 MAST CELL SURFACE GLYCOPROTEIN GP49B.
FT DOMAIN 24 268 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 239 263 POTENTIAL.
FT DOMAIN 261 335 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 125 IG-LIKE C2-TYPE 1.
FT DOMAIN 124 212 IG-LIKE C2-TYPE 2.
FT DISULFID 49 96 POTENTIAL.

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FT DIST-FIG 144 196 POTENTIAL.
FT CARBOHYD 233 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPIC 232 232 G -> D (in isoform GP49B2).
FT VARSPIC 233 232 /Frid=VSP_002510.
FT VARSPIC 233 271 Missing (in isoform GP49B2).
FT VARSPIC 271 /Frid=VSP_002511.
SQ SEQUENCE 335 AA; 37544 MW; 6005186D524E7876 CRC64;

Query Match 17.8%; Score 317.5; DB 1; Length 335;
Best Local Similarity 34.0%; Pred. No. 1.8e-16;
Matches 84; Conservative 36; Mismatches 104; Indels 23; Gaps 6;

CY 6 TALECGLCQ-GRVPAQSGFLPRPSJQALPSSLVPLEKPYTLRCQGPVGLYRLKLS 64
DB 6 TLLYLGLLEPRITAVQAGHCPKPIIWAEPGVIAAYTSVITWQSGWGAQYHYLYREKS 65
CY 65 SRVGD-----QAVLFIPAMKRSLAGRYGSGYQNSLNLPSCLFLVATGVPAKPS 115
DB 66 VNPMDTVPLEFTNKAKFNIPSMITTSYAGIKYVESAGFSEHSDAVELVMTGAYENPS 125
CY 116 LSAQPGAVSSSGEVTLQQCTRYGFDGFALYREG -----DPAKYKPRKVPASFP 167
DB 126 LSVVPSNVTSGVSISSQSSSLVFGPFLTLQEGKHLSWTLDSCHQANQPSV--ATFVL 183
CY 168 ITVTAHSGTYRQVSPSSRDPVINSAPDFLELVVGTSTVTSRSLPTPPSSVAHFESEAT 227
DB 184 EAVTNHNGTFRGVYFRNRPQVMSKPSNLDLYSETK-DCSSTPTE--DGLETYQKTL 240
CY 228 ABLTVSF 234
DB 241 TGVVVSF 247

RESULT 13
K255_HUMAN
ID K255_HUMAN STANDARD; PRT; 304 AA.
AC Q14953;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Killer cell immunoglobulin-like receptor 2B5 precursor (MHC class I
DE NK cell receptor) (Natural killer associated transcript 3) (NKAT3).
GN KIR2D5 OR NKAT9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
CX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=96270004; PubMed=8662091;
RA Doehring C., Samaridis C., Colonna M.;
RT "Alternatively spliced forms of human killer inhibitory receptors."
RL Immunogenetics 44:227-230(1996).
CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
CC DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -----
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CC -----
DR EMBL: L76672; AAR36600.1; -
DR HSSP: P43626; INKR.
DR Genex: HGNC:6337; KIR2D5.
DR MIM: 604956; -
DR GO: GO:0005887; C:integral to plasma membrane; NAS.

```

DR GO:00030110; FcHLA-C specific inhibitory MHC class I recep. NAS.
 DR GO:00030355; P:immune response; NAS.
 DR InterPro: IPR003593; IG.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF00347; IG_2.
 DR SMART: SM00409; IG_1.
 DR PROSITE: PSS0835; IG-LIKE; FALSE NEG.
 KM Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
 KM Repeat; Multigene family.
 FT SIGNAL 1 21
 FT CHAIN 22 304
 FT DOMAIN 22 245
 FT TRANSMEM 246 264
 FT DOMAIN 265 304
 FT DOMAIN 42 107
 FT DOMAIN 142 205
 FT DISULFID 49 100
 FT DISULFID 149 198
 FT CARBOHYD 67 67
 FT CARBOHYD 84 84
 FT CARBOHYD 178 178
 FT CARBOHYD 223 223
 SQ SEQUENCE 304 AA; 33644 MW; F0BD73BFA3DE35DB CRC64;

Query Match 17.2%; Score 307; DB 1; Length 304;
 Best Local Similarity 29.6%; Pred. No. 9,4e-16;
 Matches 88; Conservative 34; Mismatches 97; Indels 78; Gaps 8;

QY 27 KPSIALPSSLPLEKPVTLRCGPVGVLYRLEKLSRRYDCAV-----LF 75
 DB 28 KPSIALPSSLPLEKPVTLRCGPVGVLYRLEKLSRRYDCAV-----LF 75
 QY 76 PAKKSLAGRYRC-----SYNGSLWSLPSDQLELVATGVFAKPSLSAQGPAPVSSG 128
 DB 88 GRMQLAGTVCYRCYGVTHSPYQ---LSAPSDLDIVTGLYEKPSLPAGPPTVLAGE 143
 QY 129 CVTLQCFRYGFDQALYKSGDAPYKNP-----ERVYASFPITVTAAHSGTYPCYSF 183
 DB 144 SVTLSCSSRSSYVYHLSRSGEAEHRRLPAGPKVNRTPQADSPDLPAT--HGAAYRCFCS 201
 QY 184 SSRDPYLSAPSDPELVATGVSTPSPRLPTSPSSVAEFSTAEELTVSTFKKVTTER 243
 DB 202 FRDSPYEWKSSDPLLVSTGNSSKSWSPTEPSSS----- 237
 QY 244 SRSTSPKESDSPAGPARQYVTKNLRICLSAVLT---ILLAGPLAEQMSRRX 286
 DB 236 ---TGNPRH-----LHVLTGTSVKLPFTILLFLLHRCSSMKR 273

RESULT 14
 K2S3_HUMAN STANDARD; PRT; 304 AA.
 AC 014952; 020644;
 DT 01-NOV-1997 (rel. 35, Created)
 DT 01-NOV-1997 (rel. 35, Last sequence update)
 DT 15-SEP-2003 (rel. 42, Last annotation update)
 DE Killer cell immunoglobulin-like receptor 2DS3 precursor (MHC class I
 NK cell receptor) (Natural killer associated transcript 7) (NKAT-7).
 GN KIR2DS3 OR NKAT7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN 1;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96270004; Pubmed=8662091;
 RA Doering C., Samaridis J., Colonna M.;
 RT "Alternatively spliced forms of human killer inhibitory receptors.";
 RL Immunogenetics 44:227-230(1996).
 RC TISSUE=Lymphoid;

RA Biassoni R.;
 RL Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.
 CC 1. FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR RNA C ALLELES.
 CC DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
 CC 1. SUBCELLULAR LOCATION: type 1 membrane protein.
 CC 1. SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC 1. SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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DR EMBL: L76670; AAB36598.1; -;
 DR EMBL: X97231; CA665570.1; -;
 DR HSSP: P43626; INKR.
 DR Genew; HGNC:6335; KIR2DS3.
 DR MIM: 604954; -;
 DR GO:0005887; C: integral to plasma membrane; TAS.
 DR GO:0003822; F: MHC-interacting protein; TAS.
 DR GO:0006968; P: cellular defense response; TAS.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF0047; IG_2.
 DR SMART: SM00409; IG_1.
 DR PROSITE: PSS0835; IG-LIKE; FALSE NEG.
 KM Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
 KM Repeat; Multigene family.
 FT SIGNAL 1 21
 FT CHAIN 22 304
 FT DOMAIN 22 245
 FT TRANSMEM 246 264
 FT DOMAIN 265 304
 FT DOMAIN 42 107
 FT DOMAIN 142 205
 FT DISULFID 49 100
 FT DISULFID 149 198
 FT CARBOHYD 67 67
 FT CARBOHYD 84 84
 FT CARBOHYD 178 178
 SQ SEQUENCE 304 AA; 33717 MW; 80693F78844F9E7E CRC64;

Query Match 16.7%; Score 299; DB 1; Length 304;
 Best Local Similarity 35.2%; Pred. No. 3.7e-15;
 Matches 87; Conservative 27; Mismatches 93; Indels 40; Gaps 9;

QY 1 MSPPPTALFCGL--CGRVPAOSGRLPKPSLQALPSSLPLEKPVTLRCGPVGVLYR 58
 DB 1 KSLMVISYACVGFFWLQGAMP-HEGFRKPSLLAHGRLYKSEETVTLQNSDVMFHL 59
 QY 59 DEKSSSRYPD-----QAVLFPAMKPSLAGRYEC-----SYNGSLWSL 98
 DB 60 LHR--EGTFRNCLRLGHEHIDSVKANFSIGMRQDLAGTVCYGVFHPSPYQ---FSA 113
 QY 99 PSDQLELVATGVFAKPSLSAQGPAPVSSGQVYTLCCQTRVGFQFALYKSD-----P 151
 DB 114 PSDPLDIVTGLYEKPSLSAQGPPTVLAGESTLSGSSWSGYDMYHLSDEGAHERFSA 173
 QY 152 APYKNPKNVRSAPFIIITVLAHSGTYRCYGFSSSRDPYLSAPSDPELVATGVSTPSPR 211
 DB 174 GPKNGT--FGADPPL--GPAVGCTYRCGSGFHDSPYEWKSSDPLLVSTGNPSNSWF 229
 QY 212 LPTEPPS 218
 DB 230 SPTSPSS 236

RESULT 15
 G49A_MOUSE

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ID      G49A_MOUSE      STANDARD:      PRT:      303 AA.
AC      Q61450;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Mast cell surface glycoprotein GP49A precursor.
GN      GP49A OR GP49.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX      NCBI_TaxID:10090;
RN      [1]
RP      SEQUENCE FROM N.A. AND SEQUENCE OF 24-45.
RC      STRAIN=BALB/C; TISSUE=Bone marrow;
RX      MEDLINE=9;1340742; PubMed=1714901;
RA      Arm J.P., Garish M.F., Reynolds D.S., Scott H.C., Gartner C.S.,
RA      Austen K.F., Katz H.R.;
RT      "Molecular cloning of gp49, a cell-surface antigen that is
RT      preferentially expressed by mouse mast cell progenitors and is a new
RT      member of the immunoglobulin superfamily.";
RL      J. Biol. Chem. 266:15966-15973(1991).
CC      -1- FUNCTION: MAY PLAY A ROLE IN CELL-CELL OR CELL-CYTOKINE
CC      INTERACTIONS DURING THE DEVELOPMENT OF MAST CELLS.
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to licenses@isb-sib.ch).
CC      -----
DR      EMBL; M65027; AAA37479.1; -.
DR      PIR; A40807; A40807.
DR      HSSP; P43626; INKR.
DR      MGD; MG1:102702; GP49A.
DR      InterPro; IPR007110; Ig_Like.
DR      PROSITE; PS00835; IG_LIKE; 1.
KW      Signal; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat.
FT      SIGNAL      1      23
FT      CHAIN      24      303
FT      DOMAIN      24      238      VAST CELL SURFACE GLYCOPROTEIN GP49A.
FT      TRANSMEM      239      260      EXTRACELLULAR (POTENTIAL).
FT      DOMAIN      261      303      POTENTIAL.
FT      DOMAIN      42      125      CYTOPLASMIC (POTENTIAL).
FT      DOMAIN      124      212      IG-LIKE C2-TYPE 1.
FT      DOMAIN      124      198      IG-LIKE C2-TYPE 2.
FT      DISULFID      49      98      POTENTIAL.
FT      DISULFID      144      196      POTENTIAL.
FT      CARBOHYD      79      79      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD      133      133      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD      191      191      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ      SEQUENCE      303 AA; 34194 MW; D165639BFB9C40D CRC64;

```

Query Match	16.28;	Score 289.5;	DB 1;	Length 303;
Best Local Similarity	32.48;	Pred. No. 1.8e-14;		
Matches 81;	Conservative 35;	Mismatches 105;	Indel's 29;	Gaps 6;

QY 6 TATFCLGCT--GRVPRKSGFLPKRPSLCLALPSSLSLVELEKPVTLRCCQPPGVNLYRDEKLSS 64
DB 6 TALLYLALATLEPRTAVQAGHLPKRTIWAEPQSVIAATSVLIWQGSWEACYYTIDKKS 65
QY 65 SRVQDAV-----LFPAKRSLAGRYRQSYNGSLMSLSDQLELVAATGVFAKPS 115
DB 66 VNFWDTEVLELRNKKIKERIRMTASVAGIYNQYKSAAGFSHSDAMELMTGVENPS 125
QY 116 LSAQPSRAVSSGGDVTLCCQTRVGFDFALYKSGDAPYKNPKR-----YAS 164
DB 126 LSVPPSSAVTSGVSTSFRCSSSTLFSRFLIQG-----KAGLSVTLDSQHQAQPTHT 180
QY 165 PRLITVTAASIGTYRCYSPSSRDPLYWSAFSDPLELVVGTSTVTSRLPTPEPSSVAEFS 224

2b 181 EVLDVAPNHNNGTFRGYGFRNRPQVWSKPSNSLJLMISEK-EQSCTPTE--GGEITYQ 237
 2c 225 EATAELTVSF 234
 2d 238 KILIGVLVSF 247

Search completed: October 23, 2003, 09:42:13
Job time : 27 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

CM protein - protein search, using sw model

Run on: October 23, 2003, 09:18:24 : Search time 97 Seconds

(without alignments)
901.834 Million cell updates/sec

Title: US-09-503-387-3

Perfect score: 1786

Sequence: 1 XSPSPALAFGLGUCUGRPA.....XSHGGQDGRQDVHSRSLCS 339

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 630525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_ornithine:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_protist:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rv129:*
- 16: sp_bacteriophage:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1786	100.0	339	4	Q9U1F2
2	1676	93.8	321	4	Q9HCH7
3	1355	75.9	620	4	Q9HCH6
4	500	28.0	447	4	Q8NHJ6
5	499	27.3	444	4	Q8NHJ7
6	498	27.3	444	4	Q15468
7	498	27.3	444	4	Q8NHJ5
8	498	27.3	444	4	Q75021
9	478	26.8	461	6	Q8M122
10	477	26.7	289	4	Q75018
11	469	26.3	325	4	Q92035
12	464	26.0	631	6	Q8M123
13	453	25.7	304	4	Q76036
14	455	25.5	325	4	Q92034
15	455	25.5	325	4	Q8C567
16	455	25.5	645	6	Q8M125

17	454	25.4	631	4	Q15471	Q15471 homo sapien
18	449	25.1	631	4	Q75022	Q75022 homo sapien
19	447.5	25.1	287	4	Q76016	Q76016 homo sapien
20	443.5	24.8	306	6	Q8M128	Q8M128 macaca mula
21	443	24.8	307	6	Q8M129	Q8M129 macaca mula
22	441.5	24.7	460	6	Q8M124	Q8M124 pan troglod
23	441	24.7	466	4	Q8M149	Q8M149 homo sapien
24	441	24.7	483	4	Q75020	Q75020 homo sapien
25	440.5	24.7	306	6	Q95039	Q95039 macaca fusc
26	438.5	24.6	489	4	Q75019	Q75019 homo sapien
27	436	24.4	305	6	Q8M127	Q8M127 macaca mula
28	435.5	24.4	305	6	Q8M126	Q8M126 macaca mula
29	435	24.4	491	4	Q8M160	Q8M160 homo sapien
30	434	24.3	597	4	Q8M168	Q8M168 homo sapien
31	434	24.3	598	4	Q8M173	Q8M173 homo sapien
32	434	24.3	598	4	Q75017	Q75017 homo sapien
33	433	24.2	598	4	Q8M167	Q8M167 homo sapien
34	429	24.0	590	4	Q75023	Q75023 homo sapien
35	426.5	23.9	264	6	Q28109	Q28109 bos taurus
36	425.5	23.8	650	4	Q75024	Q75024 homo sapien
37	424.5	23.8	643	6	Q8M127	Q8M127 pan troglod
38	424.5	23.8	662	6	Q8M126	Q8M126 pan troglod
39	422	23.6	336	6	Q8M165	Q8M165 bos taurus
40	421.5	23.6	650	4	Q8M116	Q8M116 homo sapien
41	421.5	23.6	651	4	Q8M119	Q8M119 homo sapien
42	421.5	23.6	651	4	Q8M118	Q8M118 homo sapien
43	421.5	23.6	652	4	Q75025	Q75025 homo sapien
44	416.5	23.3	420	4	Q8M103	Q8M103 homo sapien
45	416.5	23.3	420	4	Q8M151	Q8M151 homo sapien

ALIGNMENTS

RESULT 1

Q9U1F2 PRELIMINARY: PRT; 339 AA.

Q9U1F2

AC Q9U1F2: 01-MAY-2000 (TREMBLrel. 13, Created)

BT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAY-2003 (TREMBLrel. 23, Last annotation update)

DE Platelet glycoprotein VI precursor (Platelet glycoprotein VI-1).

GN GPVI.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Miura Y.;

RT "Platelet glycoprotein VI-1";

RU Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RX PubMed=11027634;

RA Ezumi Y., Uchiyama T., Takayama H.;

RT "Molecular cloning, genomic structure, chromosomal localization, and

RU alternative splicing forms of the platelet collagen receptor

RI glycoprotein VI-1";

RU Biochem. Biophys. Res. Commun. 277:27-36(2000).

DR EXBL: AB035073; DAA89353.1; -

DR EXBL: AB043619; BAB12245.1; -

DR HSP: P43626; INK.

DR InterPro: IPR03599; IG.

DR InterPro: IPR03006; -IG_MHC.

DR Pfam: PF00047; IG_2.

DR SMART: SM00409; IG_2.

RN SIGNAL

FT SIGNAL 1 20 POTENTIAL.

FT CHAIN 21 339 POTENTIAL.

SC SEQUENCE 339 AA; 36923 MW; 4237576E95E030CC CRC64;

Query Match: 100.0%; Score 1786; DB 4; Length 339;

Best Local Similarity: 100.0%; Pred. No. 2,8e-146;
Matches: 339; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

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QY 1 MSPSPFALFCGLGCGRVPAQSGPLPKPSLQALPSSLVPLEKPYTLRCQGPVGLYRL 60
DB 1 MSPSPFALFCGLGCGRVPAQSGPLPKPSLQALPSSLVPLEKPYTLRCQGPVGLYRL 60
QY 61 KLSSTRYQDQAVLFTFAMKRSLAGRYRCSYQNGSLMSLPDQLELVATGVFAKPSLSAQP 120
DB 61 KLSSTRYQDQAVLFTFAMKRSLAGRYRCSYQNGSLMSLPDQLELVATGVFAKPSLSAQP 120
QY 121 GPAVSSGGDVTLQCCQTRYGFDQFALYKEGDPAPYKNERWYRASFPITVTAAHSGTYRC 180
DB 121 GPAVSSGGDVTLQCCQTRYGFDQFALYKEGDPAPYKNERWYRASFPITVTAAHSGTYRC 180
QY 191 YSFSSRDPLYLMSAPSDPLELVVTGTSVTPSRPLETPSSVAEFSSEATAELTYSFTNKVFT 240
DB 191 YSFSSRDPLYLMSAPSDPLELVVTGTSVTPSRPLETPSSVAEFSSEATAELTYSFTNKVFT 240
QY 241 TETSRSLTTSFKESDSPAGPARQYTKGNLVRIQCAVILITLACFLAEDWHRKRRLRH 300
DB 241 TETSRSLTTSFKESDSPAGPARQYTKGNLVRIQCAVILITLACFLAEDWHRKRRLRH 300
QY 301 RGRAVGRPLPLPPLPQTRKSHSGDGGRCQDVHSGSLCS 339
DB 301 RGRAVGRPLPLPPLPQTRKSHSGDGGRCQDVHSGSLCS 339

```

RESULT 2

Q9HCN7

PRELIMINARY; PRT; 321 AA.

```

AC Q9HCN7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created);
DT 01-MAR-2003 (TrEMBLrel. 16, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Platelet glycoprotein VI 2.
GN GPIIb.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=20483673; PubMed=11027634;
RA Ezumi Y., Uchiyama T., Takayama H.;
RT "Molecular cloning, genomic structure, chromosomal localization, and
RT alternative splice forms of the platelet collagen receptor
RT glycoprotein VI."
RL Biochem. Biophys. Res. Commun. 277:27-36(2000).
DR EMBL: AB043820; BAB12246.1; .
DR HSSP: P43626; INKR.
DR InterPro: IPR003593; IG.
DR Pfam: PF00347; IG_2.
DR SMART: SM00409; IG_2.
DR SEQUENCE 321 AA; 35158 MW; 53F8F88945958345 CRC64;

```

Query Match

93.8%; Score 1676; DB 4; Length 321;
Best Local Similarity 94.7%; Pred. No. 8.4e-137;
Matches: 321; Conservative: 0; Mismatches: 0; Indels: 18; Gaps: 0;

```

QY 1 MSPSPFALFCGLGCGRVPAQSGPLPKPSLQALPSSLVPLEKPYTLRCQGPVGLYRL 60
DB 1 MSPSPFALFCGLGCGRVPAQSGPLPKPSLQALPSSLVPLEKPYTLRCQGPVGLYRL 60
QY 61 KLSSTRYQDQAVLFTFAMKRSLAGRYRCSYQNGSLMSLPDQLELVATGVFAKPSLSAQP 120
DB 61 KLSSTRYQDQAVLFTFAMKRSLAGRYRCSYQNGSLMSLPDQLELVATGVFAKPSLSAQP 120
QY 121 GPAVSSGGDVTLQCCQTRYGFDQFALYKEGDPAPYKNERWYRASFPITVTAAHSGTYRC 180
DB 121 GPAVSSGGDVTLQCCQTRYGFDQFALYKEGDPAPYKNERWYRASFPITVTAAHSGTYRC 180

```

191 YSFSSRDPLYLMSAPSDPLELVVTGTSVTPSRPLETPSSVAEFSSEATAELTYSFTNKVFT 240
191 YSFSSRDPLYLMSAPSDPLELVVTGTSVTPSRPLETPSSVAEFSSEATAELTYSFTNKVFT 222

241 TETSRSLTTSFKESDSPAGPARQYTKGNLVRIQCAVILITLACFLAEDWHRKRRLRH 300
223 TETSRSLTTSFKESDSPAGPARQYTKGNLVRIQCAVILITLACFLAEDWHRKRRLRH 282

301 RGRAVGRPLPLPPLPQTRKSHSGDGGRCQDVHSGSLCS 339
283 RGRAVGRPLPLPPLPQTRKSHSGDGGRCQDVHSGSLCS 321

RESULT 3

Q9HCN6

PRELIMINARY; PRT; 620 AA.

```

AC Q9HCN6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created);
DT 01-MAR-2003 (TrEMBLrel. 16, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Platelet glycoprotein VI-3.
GN GPIIb.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=20483673; PubMed=11027634;
RA Ezumi Y., Uchiyama T., Takayama H.;
RT "Molecular cloning, genomic structure, chromosomal localization, and
RT alternative splice forms of the platelet collagen receptor
RT glycoprotein VI."
RL Biochem. Biophys. Res. Commun. 277:27-36(2000).
DR EMBL: AB043821; BAB12247.1; .
DR HSSP: P43626; INKR.
DR Genew: HGNC:4398; GP6.
DR InterPro: IPR003593; IG.
DR Pfam: PF00347; IG_2.
DR SMART: SM00409; IG_2.
DR SEQUENCE 620 AA; 67308 MW; F8B564C5F879615 CRC64;

```

Query Match

95.0%; Score 1355; DB 4; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.2e-109;
Matches: 259; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

```

QY 1 MSPSPFALFCGLGCGRVPAQSGPLPKPSLQALPSSLVPLEKPYTLRCQGPVGLYRL 60
DB 1 MSPSPFALFCGLGCGRVPAQSGPLPKPSLQALPSSLVPLEKPYTLRCQGPVGLYRL 60
QY 61 KLSSTRYQDQAVLFTFAMKRSLAGRYRCSYQNGSLMSLPDQLELVATGVFAKPSLSAQP 120
DB 61 KLSSTRYQDQAVLFTFAMKRSLAGRYRCSYQNGSLMSLPDQLELVATGVFAKPSLSAQP 120
QY 121 GPAVSSGGDVTLQCCQTRYGFDQFALYKEGDPAPYKNERWYRASFPITVTAAHSGTYRC 180
DB 121 GPAVSSGGDVTLQCCQTRYGFDQFALYKEGDPAPYKNERWYRASFPITVTAAHSGTYRC 180
QY 191 YSFSSRDPLYLMSAPSDPLELVVTGTSVTPSRPLETPSSVAEFSSEATAELTYSFTNKVFT 240
DB 191 YSFSSRDPLYLMSAPSDPLELVVTGTSVTPSRPLETPSSVAEFSSEATAELTYSFTNKVFT 240
QY 241 TETSRSLTTSFKESDSPAG 259
DB 241 TETSRSLTTSFKESDSPAG 259

```

RESULT 4

Q8NHJ6

PRELIMINARY; PRT; 447 AA.

01-OCT-2002 (TrEMBLrel. 22, Created);

```

LT 01-OCT-2002 (TREMBLrel. 22, Last sequence update);
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update);
DE Leukocyte immunoglobulin-like receptor-5.
GN LILRB5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Canavez F.C.;
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF283988; AAC36592.1;
DR InterPro: IPR003006; I9_MHC.
DR Pfam: PF00047; I9; 2.
KM Receptor.
SQ SEQUENCE 447 AA; 49193 MW; 6B1E83E2B31C7614 CRC64;

Query Match: 28.0%; Score 500; DB 4; Length 447;
Best Local Similarity 36.0%; Pred. No. 6,3e-35;
Matches 133; Conservative 41; Mismatches 127; Indels 68; Gaps 9;

CY 1 MSPPTALFCLGLCLG-RVPAQSGPLPKPSLQAPSSLVLEKPVTLRCQGFPGVDLYRL 59
DB 1 MIPPTALCLGLSLGPRTHMQAGPLPKPTLWAEPSGVSISWNSVTIMCQGLEAREYRL 60
CY 60 EKLSSSRVQD-----QAVFFIPAMKRLAGRYRCISYONGSJKSLPDCLELVATGV 110
DB 61 EKESPPAPKDRQNPLEPKNKARSLPSMTEDYAGRYRCYRSPVGMSCPSDPLELVMTGA 120
CY 111 FAKPSLSAQPGPAVSSGGDVTLCCQTRYGFDPALYKGDPAFY-----KNFERWYRASF 165
DB 121 YSKPTLSALPSPLVTSKSVTLCCQSRSPMDTFLIKERAAHPLHLRSEHGAQQAEEF 180
CY 166 PIIIVTAHSGTYRCYSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSE 225
DB 181 PMSPTSVHGGTYRCFSHGFSHYLLSHPSDPLELVSGSLDPRRPSPT----- 229
CY 226 ATAELIVSFTNKVFTTETSRTSPKESDSPAGPARQYTKG-----NIVRICGAVI 279
DB 230 -----RSVSTAAGPEDQPLMPTGVSFPHSGLRHHEVLIGLVVSIL 270
CY 280 LILLAGF-LAEQWHSRRKR-LRHGRVQRPPLPPLPQTRKSHGGQDGRQ----- 330
DB 271 LLSLLFLLLQHWKQKHRTLAQROADFQRPGAABEP-----KDGGLQRRSSPAA 322
CY 331 DVHSRGLCS 339
DB 323 DVQGENFCA 331

RESULT 5
OS NCBI7
ID OSNC17 PRELIMINARY; PRT; 448 AA.
AC OSNC17;
DT 01-OCT-2002 (TREMBLrel. 22, Created);
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update);
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update);
DE Leukocyte immunoglobulin-like receptor, subfamily 5 (with TM and ITIM domains), member 4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC026309; AAH26309.1;
DR InterPro: IPR003006; I9_MHC.
DR Pfam: PF00047; I9; 2.
KM Receptor.

```

```

SQ SEQUENCE 448 AA; 49303 MW; A6155D29E7D89812 CRC64;

Query Match: 27.9%; Score 499; DB 4; Length 448;
Best Local Similarity 36.0%; Pred. No. 8,3e-35;
Matches 133; Conservative 41; Mismatches 127; Indels 68; Gaps 9;

CY 1 MSPPTALFCLGLCLG-RVPAQSGPLPKPSLQAPSSLVLEKPVTLRCQGFPGVDLYRL 59
DB 1 MIPPTALCLGLSLGPRTHMQAGPLPKPTLWAEPSGVSISWNSVTIMCQGLEAREYRL 60
CY 60 EKLSSSRVQD-----QAVFFIPAMKRLAGRYRCISYONGSJKSLPDCLELVATGV 110
DB 61 EKESPPAPKDRQNPLEPKNKARSLPSMTEDYAGRYRCYRSPVGMSCPSDPLELVMTGA 120
CY 111 FAKPSLSAQPGPAVSSGGDVTLCCQTRYGFDPALYKGDPAFY-----KNFERWYRASF 165
DB 121 YSKPTLSALPSPLVTSKSVTLCCQSRSPMDTFLIKERAAHPLHLRSEHGAQQAEEF 180
CY 166 PIIIVTAHSGTYRCYSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSE 225
DB 181 PMSPTSVHGGTYRCFSHGFSHYLLSHPSDPLELVSGSLDPRRPSPT----- 229
CY 226 ATAELIVSFTNKVFTTETSRTSPKESDSPAGPARQYTKG-----NIVRICGAVI 279
DB 230 -----RSVSTAAGPEDQPLMPTGVSFPHSGLRHHEVLIGLVVSIL 270
CY 280 LILLAGF-LAEQWHSRRKR-LRHGRVQRPPLPPLPQTRKSHGGQDGRQ----- 330
DB 271 LLSLLFLLLQHWKQKHRTLAQROADFQRPGAABEP-----KDGGLQRRSSPAA 322
CY 331 DVHSRGLCS 339
DB 323 DVQGENFCA 331

RESULT 6
OS NCBI7
ID OS15468 PRELIMINARY; PRT; 448 AA.
AC OS15468;
DT 01-JAN-1998 (TREMBLrel. 05, Created);
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update);
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update);
DE Monocyte inhibitory receptor precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Arm J.P., Nwanke C., Austen K.F.;
RT "Molecular identification of a novel family of human immunoglobulin superfamily members that possess immunoreceptor tyrosine-based inhibitory motifs and homology to the mouse gp49B1 inhibitory receptor."
RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U91925; AAB68665.1;
DR HSSP: P43626; INXR.
DR Genew: HGNC:6608; LILRB4.
DR InterPro: IPR003599; I9.
DR InterPro: IPR003006; I9_MHC.
DR Pfam: PF00047; I9; 2.
DR SMART: SM00439; I9; 1.
DR Receptor; Signal.
KM SIGNAL
FT CHAIN 24 448 MONOCYTE INHIBITORY RECEPTOR.
SQ SEQUENCE 448 AA; 49297 MW; 7631E24A82EA1399 CRC64;

Query Match: 27.9%; Score 498; DB 4; Length 448;
Best Local Similarity 36.0%; Pred. No. 1e-34;
Matches 133; Conservative 41; Mismatches 127; Indels 68; Gaps 9;

CY 1 MSPPTALFCLGLCLG-RVPAQSGPLPKPSLQAPSSLVLEKPVTLRCQGFPGVDLYRL 59
DB 1 MIPPTALCLGLSLGPRTHMQAGPLPKPTLWAEPSGVSISWNSVTIMCQGLEAREYRL 60

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```
DB 1 MIPFTALLCLGLSLGPRTHMAGPLPKPTLMAEPGVSISGNSVTIKCGTLEAREVEL 60
CY 60 EKLSSSRYQD-----QAVLFPAMKRSIAGRYRCYQNGSLWLSLPSDQLELVATGV 110
DB 61 DKEESPAPFWRQNPLEPKKARFSPSMTEDEYAGRYRCYRSPVQWGSQPSDPLELVMTGA 120
CY 111 FAKPSLSAQPGPAVSSGGCVTLCCQTRYGFDQFALYKEGDPAPY-----KNPERWYRASF 165
DB 121 YSKPTLSALPSPLVTSKSVTLCCQSRSPMDTFLIKERAAHFLHTRSEHGAQCHQAEF 180
CY 166 PITTVAASGTYRCYSPSSRDPLYMSAPSDPLELVATGTSVTPSRLPTEPPSSVAAPFSE 225
DB 181 PMSPTSVHGGTYRCFSSHGFSHYLLSHPSDPLELVSGSLGPRSPPT----- 229
CY 226 ATAELTVSFTNKVFTTETSRISITSPKESDSPAQPARQVYTKG-----NLVRIQGAVI 279
DB 233 -----RSVSTAAGPEDQPLMPTGVSFHSGLRRHWEVLIGVLVWSTL 270
CY 280 LILLAGF-LAEDWHSRRKR-LRRGRGAVQRPPLPLPQTRKSHGGQDGRQ----- 330
DB 271 LLSLLFLLLQHWROGKRRTLAQROADFGRRPGAABEP-----KDQGLQRSSPAA 322
CY 331 DVHSRGLCS 339
DB 323 DVQGENFCA 331

RESULT 7
QSNHJ5
ID QSNHJ5 PRELIMINARY: PRT: 448 AA.
AC QSNHJ5:
DT 01-OCT-2002 (Tremblrel: 22, Created)
DT 01-OCT-2002 (Tremblrel: 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel: 23, Last annotation update)
DE Leukocyte immunoglobulin-like receptor 5.
GN LIR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 1:
RP SEQUENCE FROM N.A.
RX MEDLINE=2035285; Pubmed=10941837;
RA Liu W.R., Kim C., Nwankwo C., Astworth L.K., Arm J.P.;
RT "Genomic organization of the human leukocyte immunoglobulin-like
RT receptors within the leukocyte receptor complex on chromosome
RT 19q13.4."
RL Immunogenetics 51:659-669(2000).
DR EMBL: AF189768; AAG02024.1;
DR InterPro: IPR033006; IG_MHC.
DR Pfam: PF00047; Ig_2.
KW Receptor.
SQ SEQUENCE 448 AA; 49328 MW; 98310C446CEA1593 CRC64;

Query Match 27.9%; Score 498; DB 4; Length 448;
Best Local Similarity 36.0%; Pred. No. 1e-34;
Matches 133; Conservative 41; Mismatches 127; Indels 68; Gaps 3;
```

```
CY 226 ATAELTVSFTNKVFTTETSRISITSPKESDSPAQPARQVYTKG-----NLVRIQGAVI 279
DB 230 -----RSVSTAAGPEDQPLMPTGVSFHSGLRRHWEVLIGVLVWSTL 270
CY 280 LILLAGF-LAEDWHSRRKR-LRRGRGAVQRPPLPLPQTRKSHGGQDGRQ----- 330
DB 271 LLSLLFLLLQHWROGKRRTLAQROADFGRRPGAABEP-----KDQGLQRSSPAA 322
CY 331 DVHSRGLCS 339
DB 323 DVQGENFCA 331
```

```
RESULT 8
Q75021
ID Q75021 PRELIMINARY: PRT: 448 AA.
AC Q75021:
DT 01-NOV-1998 (Tremblrel: 08, Created)
DT 01-NOV-1998 (Tremblrel: 08, Last sequence update)
DT 01-MAR-2003 (Tremblrel: 23, Last annotation update)
DE Leukocyte immunoglobulin-like receptor-5.
GN LIR-5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 1:
RP SEQUENCE FROM N.A.
RA Berges L., Hsu M.-L., Fanger N., Rubin M., Cosman D.;
RL Immunol. 0:0-0(1997).
DR EMBL: AF025532; AAB87666.1;
DR HSSP: P43626; INXR.
DR InterPro: IPR003599; IG.
DR InterPro: IPR003306; IG_MHC.
DR Pfam: PF00047; Ig_2.
DR SMART: SMC0409; IG_1.
SQ SEQUENCE 448 AA; 49325 MW; 76D1E0B7A03A1399 CRC64;

Query Match 27.9%; Score 498; DB 4; Length 448;
Best Local Similarity 36.0%; Pred. No. 1e-34;
Matches 133; Conservative 41; Mismatches 127; Indels 68; Gaps 9;
```

Q8MU22
ID Q8MU22 PRELIMINARY; PRT: 481 AA.
AC Q8MU22;
DT 01-OCT-2002 (TrEMBLrel. 22, Created;
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Leukocyte immunoglobulin-like receptor e.
GN LIR-6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2155186; PubMed=11693452;
RA Canavez F.C., Young N.T., Guehlstein L.A., Ravalinger R., Khakoo S.,
RA Shum B.P., Parham P.;
RT "Comparison of chimpanzee and human leukocyte Ig-like receptor genes
RT reveals framework and rapidly evolving genes";
RJ J. Immunol. 167:5786-5794(2001).
DR EMBL; AF383169; ALU1878.1; -
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR003598; IG_MHC.
DR Pfam; PF00047; IG_4.
DR SMART; SM00409; IG_LIKE; 1.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 481 AA; 52438 MW; 3E8FC7E87245F0FC CRC64;

Query Match: 26.8%; Score 478; DB 6; Length 481;
Best Local Similarity 26.8%; Pred. No. 66-33;
Matches 136; Conservative 41; Mismatches 80; Indels 254; Gaps 9;

QY 1 MSPTALFCLGCTG-RVPAQSGPLPKPSLQALPSSLVPLEKVTLRCCGPPGVLYRL 59
DB 1 WTPILTLICLGLSGPRTHVQAGTLPKPTLMAEPGSVITQSGPVTLMCGCLETGEYRL 60
QY 60 EKLSSSRVQD-----QAVLFIPAKRSIAGRYCSYQNGSL-WSLPSDCELVATG 110
DB 61 YKESREPRDTONMEPKMKARISIPSMTEHHAGRYRCYRSPAGMSEPSDPELVATG 120
QY 111 FAKPSLSAQGPRAVSSGGVTLQCCQTRYGFDQFALYKES----- 149
DB 121 AYKPTLSALPSPVVTSGGNVTLHCVSQVAFSGFILCKEGEDHPQCNSCPETHGWSRA 180
QY 150 -----DP-----AP----- 153
DB 181 FVGVPTFSHRWTVTCYGYRNTFQVWSHPSPLEILPSGVSRKPSLTLCCGPVLAPGES 240
QY 154 -----YKNER----- 159
DB 241 LTIQCGSDVGYCRFLYKESGERDELQJFGPQQAQMSQANFTLVFVSRSHGQYROYGAH 300
QY 160 -----W----- 160
DB 301 NLSSEWSAPSDPNIILAGQFYDVSLSLOPDTVASGENTVLCCSQGCFDTLLTKEG 360
QY 161 -----YRASPIITVTAHSGTYRCYFSRSSRDVYLMASAPDPELVATG 204
DB 361 AAHPDLRIKSKYQCKYQAFPMNPVTSAAHGYRCYGSYSRPHLLSGFSDPLKLVSG 420
QY 205 TSVTPSRLPTPEPSVAEVSATAEVTSFINKVFTTTSRTTSKESDSEAGPARQY 264
DB 421 PGGGSLPPTGPPS-----TFASMAKD- 442
QY 265 YTKGNLVRICGAVILIIAGFLAEDWHSR 295
DB 443 YTVENLIRMGYAGLVVGLLFEAQHSQR 473

RESULT 10
075019
ID C75018 PRELIMINARY; PRT: 293 AA.
AC 075018;

DT 01-NOV-1998 (TrEMBLrel. 08, Created;
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Leukocyte immunoglobulin-like receptor-6b.
GN LIR-6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX EMBL; AF325529; AAB8763.1; -
RJ J. Immunol. 160:3019-3027(1997).
DR EMBL; AF325529; AAB8763.1; -
DR HSSP; P43626; INKR.
DR InterPro; IPR003599; IG_1.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_MHC.
DR Pfam; PF00047; IG_1.
DR SMART; SM00409; IG_LIKE; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 289 AA; 31623 MW; E1930C4C65AEAL19 CRC64;

Query Match: 26.7%; Score 477; DB 4; Length 289;
Best Local Similarity 38.5%; Pred. No. 37-33;
Matches 120; Conservative 46; Mismatches 104; Indels 42; Gaps 10;

QY 1 MSPTALFCLGCTG-RVPAQSGPLPKPSLQALPSSLVPLEKVTLRCCGPPGVLYRL 59
DB 1 WTPILTLICLGLSGPRTHVQAGTLPKPTLMAEPGSVITQSGPVTLMCGCLETGEYRL 60
QY 60 --EKUSS--SRVQDAV---LFIAPAKRSIAGRYCSYQNGSL-WSLPSDCELVATG 109
DB 61 YKESREPRDTONMEPKMKARISIPSMTEHHAGRYRCYRSPAGMSEPSDPELVATG 120
QY 110 VFAKPSLSAQGPRAVSSGGVTLQCCQTRYGFDQFALYKESD---PARYKNER---WYRA 163
DB 121 AYKPTLSALPSPVVTSGGNVTLHCVSQVAFSGFILCKEGEDHPQCNSCPETHGWSRA 180
QY 164 SFTPIITVTAHSGTYRCYFSRSSRDVYLMASAPDPELVATGTSVTPSRLPTPEPSVAEF 223
DB 181 IFSVGPVSPSRKWSRYCYAYDSNPVWSLPSDLELVVFGAAETLS-----PRONKSDS 235
QY 224 SEATAEITVSFTNKVFTTETSRSITTSFKESDSEAGPARQYTKGNLVRICGAVILII 283
DB 236 KAGAN-----TLSPQNKTAASRP--QDYTVENLIRMGYAGLVVVL 275
QY 284 AGFLAEDWHSR 295
DB 276 GILFFEQAHSQR 287

RESULT 11
Q9Z0H5
ID Q9Z0H5 PRELIMINARY; PRT: 325 AA.
AC Q9Z0H5;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE NKXAR.
GN AR-1 OR KILR-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10115;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Lymphoid;
RA Falco N., Cantoni C., Bottino C., Moretta L., Biasoni R.;
RT "Identification of the rat homologue of the human NKx4 triggering
RT receptor";
RJ Submitted (FEB-1999) to the EMBL/GenBank/DBS databases.
RN [2]

R2 SEQUENCE FROM N.A.
 RC STRAIN=PV3;
 RA Berg S.F., Dassen E., Westgaard T.H., Fossum S.,
 RT "Molecular characterization of KIR-1, a novel immunoglobulin-like
 RL gene in the rat, expressed by NK cells."
 DR EMBL: A701274; CAA10161.1;
 DR EMBL: AF082513; AAC69890.1;
 DR HSSP: P43626; INKR.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF00047; IG_2.
 DR SMART: SMC0409; IG_2.
 KM Receptor.
 SQ SEQUENCE 325 AA; 37178 MW; 502C1CA02F55FA4 CRC64;

Query Match 26.3%; Score 469; DB 1; Length 325;
 Best Local Similarity 37.7%; Pred. No. 2,1e-32;
 Matches 116; Conservative 38; Mismatches 116; Indels 36; Gaps 5;

QY 1 MSPPTALFCLGLCLG-RVPAQSGFLPKPSLQALPSSLVPLEKPVTLRCQGPVGLYR-59
 D6 1 MEFITLALMCLGLCLGSRINTKQCLPKPIIMAKPSIMVTKGNEVIMCGAGASAEVQL-60
 QY 59 -----LEKISSRYQDQAVLF-PAMKRLAGRYRQSYQNSLMSLPSCDEEVATGV-110
 D6 61 YFEGSFELERPKESRSMKVKVEFLSQNTSHTAG-VTCFYQSGEIMSSSNPKLVITGL-120
 QY 111 FAKESLSAQPGPAVSSGGVTLTQCCTRYGFDQFALYKEDPAPYKNSPERWYASFPITV-170
 D6 121 YDTPLMWHPGPEVLTGENVTFSCHLKATATSKPEFLKERHSHIQKYGNTCAEFTMGPV-180
 QY 171 PAISGTYRCYSFSSRPDYLMASAPDPLEVVTGTSTVPSRLTEPSSVA--EFSEATA-228
 D6 191 TPARGTYRC--FGSYNDFAWSPSPRPVTLITGVENTSLAPDPVSSLDYWEFDIST-237
 QY 225 EGVSVFTNKVFTTETSRSTTSPKESDSPAGPARVYTKNLYECLGAVILITAGVLA-288
 D6 238 -----KESGLQKTSAPWEHTAQNILRIQLACITVNAIVMWA-274
 QY 289 EDWHSRRK-296
 D6 275 EDWHSRRK-282

RESULT 12

Q8MU23

PRELIMINARY; PRT: 631 AA.

ID Q8MU23;
 AC Q8MU23;
 DT 01-OCT-2002 (TREMblrel. 22, Created)
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Leukocyte immunoglobulin-like receptor d.
 GN LIR.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN 1;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2155186; PubMed=11698452;
 RA Caravez F.C., Young N.T., Gethlein L.A., Rajalingam R., Khakoo S.I.,
 RA Sam B.P., Parham P.;
 RT "Comparison of chimpanzee and human leukocyte Ig-like receptor genes
 RT reveals framework and rapidly evolving genes."
 RT J. Immunol. 167:5786-5794(2001).
 RL EMBL: AF383168; AAL31877.1;
 DR EMBL: AF383168; AAL31877.1;
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007113; IG-like.
 DR InterPro: IPR003598; IG_2.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF00047; IG_4.
 DR SMART: SM00409; IG_4.

CR SMART: SM00408; IG_2;
 DR PROSITE: PS50835; IG_LIKE; 2.
 KM Immunoglobulin domain; Receptor.
 SQ SEQUENCE 631 AA; 69456 MW; 10E7B706D2B4DEFF CRC64;

Query Match 26.3%; Score 464; DB 6; Length 631;
 Best Local Similarity 39.5%; Pred. No. 1.4e-31;
 Matches 113; Conservative 46; Mismatches 107; Indels 20; Gaps 7;

QY 1 MSPPTALFCLGLCLG-RVPAQSGFLPKPSLQALPSSLVPLEKPVTLRCQGPVGLYR-59
 D6 1 MEFITLALMCLGLCLGSRINTKQCLPKPIIMAKPSIMVTKGNEVIMCGAGASAEVQL-60
 QY 60 EKUSSRYQD-----CAVVFIPAMKRLAGRYRQSYQNSLMSLPSCDEEVATGV-110
 D6 61 YFEGSFELERPKESRSMKVKVEFLSQNTSHTAG-VTCFYQSGEIMSSSNPKLVITGL-120
 QY 111 FAKESLSAQPGPAVSSGGVTLTQCCTRYGFDQFALYKEDPAPYKNSPERWYASFPITV-164
 D6 121 YKPEFLSALPSPVYASGAVTLRCGSGCKYCHVLYKKEGEGQPRTLDSQQLHSGFCAL-180
 QY 165 PPIITVTAHSGTYRCYSFSSRPDYLMASAPDPLEVVTGTSTVPSRLTEPSSVAEFS-224
 D6 181 PFGVPTPSHRWTPRCYVYVTVNQVWSHSPDPLFLPSGVSRRPSLLTLGSP-VLARGE-239
 QY 225 EATAEL--TVSFTNKVFTTETSRSTTSPKESDSPAGPARVYTKG-268
 D6 240 STLQCGSDVGDRFVLYKEGERDFLQRPQGPQ-AGLSQANFTLG-284

RESULT 13

Q76036

PRELIMINARY; PRT: 304 AA.

ID Q76036;
 AC Q76036;
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE NK receptor (lymphocyte antigen 94 homolog, activating NK-receptor,
 DE NK-p46.) (Mouse).
 GN NK-P46.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN 1;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98401029; PubMed=9730896;
 RA Persico A., Sivori S., Bottino C., Malaspina A., Morelli L.,
 RA Moretta L., Giasson R., Moretta A.;
 RT "Molecular cloning of Nkp46: a novel member of the immunoglobulin
 RT superfamily involved in triggering of natural cytotoxicity."
 RT J. Exp. Med. 188:953-960(1998).
 GN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC001383; CAA04714.1;
 DR EMBL: BC030265; AAH30265.1;
 DR HSSP: P43626; INKR.
 DR Genew: HGNC:6731; NCRL.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF00047; IG_1.
 KM Receptor.
 SQ SEQUENCE 304 AA; 34480 MW; FBCBDE50D2F34CD3 CRC64;

Query Match 25.7%; Score 459; DB 4; Length 304;
 Best Local Similarity 36.1%; Pred. No. 1.4e-31;
 Matches 117; Conservative 45; Mismatches 108; Indels 54; Gaps 9;

QY 1 MSPPTALFCLGLCLG-RVPAQSGFLPKPSLQALPSSLVPLEKPVTLRCQGPVGLYR-59
 D6 1 MEFITLALMCLGLCLGSRINTKQCLPKPIIMAKPSIMVTKGNEVIMCGAGASAEVQL-60


```
Db 1 MSSTLPALLCVGLCSORISAQQQLPKPFIMAEPMFVMPKREKQVTTCCQSNVGAWEYQL 60
QY 60 -----EKSSSRVQDQAVLFTPANKRSLAGRYKSYQNGSLWSPSDOL 104
Db 61 HFEGLFAVDRPKPRRINKVKF-----YIPDNMSMAGQSCCYRVGELWSPSSULD 114
QY 105 LVATGVFAKPSLSAQOPQAVSSGGCVTLQCCTRYGFDPQALYKSGDPAPYKNERWYRAS 164
Db 115 LVVTEMYDPTLSVTFPGFVLSGEKVTFCRLDTATSNVLLKSGRSSHVQSGKQVQAE 174
QY 165 FPIITVTAHSGTVRCYSPSSRPDPLWMSAPSDLELVWG-----TSVTPSRADTEPPSSV 220
Db 175 FPLGPVTTAHRGTVRC--FGSYNNHAWSPSSSEYKLVGTGDIENSTAPED-STFPACTW 231
QY 221 AEFSEATNELTVSPNKVFTTETSRSCTTSPKESDPAQPARQVYTKGNLVKCLSAVIL 290
Db 232 GTY-----LITTEIG-----LQKDH---ALWDHTAQNLRVGLAFVL 266
QY 281 ITLAGFLAEDWHSRKRRLRHGRRA 304
Db 267 VALVWFVLEDWLSRKRTRERASSRA 290
```

RESULT 14

```
Q920Q4 PRELIMINARY: PRJ: 325 AA.
AC Q920Q4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Activating receptor 1.
GN NCRI_O1994 OR MAR-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=lymphoid;
RX MEDLINE=99190527; PubMed=10092106;
RA Biassoni R., Bessino A., Bottino C., Bende D., Moretta L., Moretta A.;
RT "The murine homologue of the human NKp46, a triggering receptor
RT involved in the induction of natural cytotoxicity.";
RL Eur. J. Immunol. 29:1014-1020(1999).
DR EMBL: AJ223765; CAB39169.1; .
DR HSSP: P43626; INKR.
DR MGI: 133422; Ncr1.
DR InterPro: IPR003599; IG.
DR InterPro: IPR003006; IG_YHC.
DR Pfam: PF00047; IG_2.
DR SMART: SM00409; IG_2.
KW Receptor.
SQ SEQUENCE 325 AA; 37265 MW; ED24E48ABF22FC29 CRC64;
```

Query Match 25.5%; Score 455; DB 11; Length 325;
Best Local Similarity 38.0%; Pred. No. 3.5e-31;
Matches 117; Conservative 36; Mismatches 117; Indels 38; Gaps 6;

```
QY 1 MSPSPALFCJGLCLG-RVPAQSGPDPKPSLQALPSSLVPLEKPYTLRCQSPGCVDIYR- 58
Db 1 MDPPTALLCLGLCSORINTEKETLPKPIIAKPSIMWTNGSNVIMWQGAQASAEYQL 60
QY 59 -----LEKSSSRVQDQAVLFTPANKRSLAGRYKSYQNGSLWSPSDOLFLVATGV 110
Db 61 YFEGSFPALEPRKPRSRMKNVRFPSQMTSHTAGIYTCFYQSGELWSSKSNPLKLVITGL 120
QY 111 FAKPSLSAQOPQAVSSGGCVTLQCCTRYGFDPQALYKSGDPAPYKNERWYRASFPITV 170
Db 121 YDTENLWVYPPREVLTGENVTFFCQIKTATSKPFLIKERGSNHCQKYGNTQAPRWGPV 180
QY 171 TAAHSGTVRCYSPSSRDPYLSAPSDPLELVVGTGTSVTPSRLPTEPSSVA--EFSQATA 223
Db 181 TRAHRGTVRC--FGSYNDYAWSPSEFPVTLITGVENSSLAFTDPTSSLDYWEFDLSTN 238
```

```
QY 229 ETVSPFNKVFTEITSRSITTSPKESDPAQPARQVYTKGNLVKCLSAVILITAGFLA 268
Db 239 E-----SGLQKDS---AFWDHTQNLIRIGLACILITLVWDDT 274
QY 289 EDWHSRRK 296
Db 275 EDWLSRKR 282
```

RESULT 15

```
Q9C567 PRELIMINARY: PRJ: 325 AA.
AC Q9C567;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Lymphocyte antigen 94.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Bone;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the FANTOM Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL: AK079401; BAC37635.1; .
DR EXBL: AK079401; BAC37635.1; .
SQ SEQUENCE 325 AA; 37237 MW; 42272A976E3E3E34 CRC64;
```

Query Match 25.5%; Score 455; DB 11; Length 325;
Best Local Similarity 38.0%; Pred. No. 3.5e-31;
Matches 117; Conservative 36; Mismatches 117; Indels 38; Gaps 6;

```
QY 1 MSPSPALFCJGLCLG-RVPAQSGPDPKPSLQALPSSLVPLEKPYTLRCQSPGCVDIYR- 58
Db 1 MDPPTALLCLGLCSORINTEKETLPKPIIAKPSIMWTNGSNVIMWQGAQASAEYQL 60
QY 59 -----LEKSSSRVQDQAVLFTPANKRSLAGRYKSYQNGSLWSPSDOLELVATGV 110
Db 61 YFEGSFPALEPRKPRSRMKNVRFPSQMTSHTAGIYTCFYQSGELWSSKSNPLKLVITGL 120
QY 111 FAKPSLSAQOPQAVSSGGCVTLQCCTRYGFDPQALYKSGDPAPYKNERWYRASFPITV 170
Db 121 YDTENLWVYPPREVLTGENVTFFCQIKTATSKPFLIKERGSNHCQKYGNTQAPRWGPV 180
QY 171 TAAHSGTVRCYSPSSRDPYLSAPSDPLELVVGTGTSVTPSRLPTEPSSVA--EFSQATA 223
Db 181 TRAHRGTVRC--FGSYNDYAWSPSEFPVTLITGVENSSLAFTDPTSSLDYWEFDLSTN 238
QY 229 ETVSPFNKVFTEITSRSITTSPKESDPAQPARQVYTKGNLVKCLSAVILITAGFLA 268
Db 239 E-----SGLQKDS---AFWDHTQNLIRIGLACILITLVWDDT 274
QY 289 EDWHSRRK 296
Db 275 EDWLSRKR 282
```

Search completed: October 23, 2003, 09:40:15
Job time: 103 secs

21 Qian M, Kingsbury G;
 XX WP1; 2001-080877/09.
 DR N-PSDB; AAF29470, AAF23471.
 XX
 PT New genes encoding human platelet-expressed collagen receptor,
 PT glycoprotein VI, and its modulators, useful for preventing, treating
 PT and diagnosing hemorrhagic disorders, thrombotic diseases and
 PT immunological disorders.
 XX
 PS Claim 8: Fig 1A: 227pp; Eng-lish.
 XX
 CC The present sequence is given in a specification relating to an isolated
 CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
 CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
 CC and polypeptides and their modulators, e.g. antisense nucleic acids,
 CC ribozymes and antibodies, are useful for preventing, treating and
 CC diagnosing disorders associated with aberrant expression or activity of
 CC GPVI. These disorders include bleeding disorders
 CC (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
 CC (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
 CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
 CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
 CC infarction), immunological diseases (e.g. platelet disorder) and
 CC embryonic liver disorders. Preferably they are used to prevent acute
 CC cardiac ischaemia following angioplasty and metastatic cancers,
 CC especially of the colon and liver.
 XX
 SC Sequence 339 AA;
 Query Match 100.0%; Score 1786; DB 22; Length 339;
 Best Local Similarity 100.0%; Pred. No. 6.2e-141;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSPSPFALFCLGLGCRVPAQSGPLPKPSLQALPSLSLVPLEKPTLRGCGPPGVLYRLF 50
 DB 1 MSPSPFALFCLGLGCRVPAQSGPLPKPSLQALPSLSLVPLEKPTLRGCGPPGVLYRLF 60
 QY 61 KLSRSRYQDQAVLFIAPAKRSJAGRIKCSYONSLNSJSDQLELVATGVFAKESLSAQF 120
 DB 61 KLSRSRYQDQAVLFIAPAKRSJAGRIKCSYONSLNSJSDQLELVATGVFAKESLSAQF 120
 QY 121 GFAVSSGGDVTLCCQTRVGFQFALYKEGDPAPKPKPEYKASPTITVTANSGTYRC 180
 DB 121 GFAVSSGGDVTLCCQTRVGFQFALYKEGDPAPKPKPEYKASPTITVTANSGTYRC 180
 QY 181 YSFSSRRPYLWSAPSPDLNVTGTSTVTPSRPLTPRSSVAEFSATAEITVSTNKVFT 240
 DB 181 YSFSSRRPYLWSAPSPDLNVTGTSTVTPSRPLTPRSSVAEFSATAEITVSTNKVFT 240
 QY 241 TETSRSTTSPEKESDSSAGAFARQYVTKNLRICGAVIJJLLAGFLAEDWHSRKRLLH 300
 DB 241 TETSRSTTSPEKESDSSAGAFARQYVTKNLRICGAVIJJLLAGFLAEDWHSRKRLLH 300
 QY 301 RGRAVGRPLPLPLPQTRKSHGQGGGQGDVHSRGLCS 339
 DB 301 RGRAVGRPLPLPLPQTRKSHGQGGGQGDVHSRGLCS 339
 RESULT 2
 ABU11221
 ID ABU11221 standard; Protein: 339 AA.
 XX
 AC ABU11221;
 XX
 DT 06-FEB-2003 (first entry)
 XX
 DE Human TANGO 268 protein.
 XX
 KW Human; mouse; variable heavy; VH; antigen; cancer;
 KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;
 KW TANGO 268; extracellular matrix; collagen; platelet release;
 KW proliferation; migration; embryogenesis; inflammation; thrombosis;

KW degeneration; thrombocytopaenia; antibody; thrombotic disorder;
 KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
 KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
 KW cardiovascular disease; angina pectoris; myocardial infarction;
 KW coronary restenosis; atherosclerosis; immunological disorder;
 KW developmental disorder; embryonic disorder; liver disorder;
 KW cerebral vascular disease; venous thromboembolism disease.
 XX
 OS Homo sapiens.
 XX
 PM WO200280968-A1.
 XX
 PD 17-OCT-2002.
 XX
 PP 09-APR-2002; 2002WO-US11122.
 XX
 PR 09-APR-2001; 2001US-0829495.
 XX
 PA (MILLER) WILLENITLY PHARM INC.
 XX
 PI Busfield SC, Willeva C, Jandro-Ferrus M, Vainochucker W, Gill DS;
 PI Qian M, Kingsbury G;
 XX
 DR WP1; 2003-058477/05.
 DR P-PSDB; ABX17291, ABX17290.
 XX
 PT Novel substantially purified antibody immunospecifically binding to
 PT TANGO 268 antigen, useful for treating bleeding disorders such as
 PT thrombocytopaenia, stroke, ischaemia, pulmonary embolism, atherosclerosis
 PT
 XX
 PS Disclosure; Figure 1; 235pp; English.
 XX
 CC This invention relates to a novel purified antibody comprising a
 CC variable heavy (VH) complementarity determining region (CDR1, VH CDR2
 CC or VH CDR3) or variable light (VL) CDR1, VL CDR2 or VL CDR3, and
 CC immunospecifically binding to a TANGO 268 (also referred as glycoprotein
 CC VI (GPVI)) antigen. The antibodies of the invention act to decrease or
 CC block TANGO 268 binding to extracellular matrix components, or as a
 CC collagen or platelet release and aggregation blocker. The antibodies of
 CC the invention are useful for modulating proliferation, migration,
 CC morphology, differentiation and/or function of megakaryocytes and
 CC platelets, including during development e.g. embryogenesis, modulating
 CC leukocyte-platelet and platelet-endothelium interactions in
 CC inflammation and/or thrombosis, and modulating platelet aggregation and
 CC degranulation. They are also useful for modulating disorders associated
 CC with abnormal or aberrant megakaryocyte and/or platelet proliferation,
 CC migration, morphology, differentiation and/or function, e.g. bleeding
 CC disorders such as thrombocytopaenia. Other diseases which may be
 CC modulated by these antibodies are thrombotic disorders, cerebral
 CC vascular diseases (e.g. stroke and ischaemia), venous thromboembolism
 CC diseases (e.g. diseases involving leg swelling, pain and ulceration,
 CC pulmonary embolism, etc), coronary diseases (e.g. cardiovascular
 CC diseases including angina pectoris, myocardial infarction, coronary
 CC restenosis, atherosclerosis, etc), immunological disorders, coronary
 CC developmental disorders, embryonic disorders, liver disorders, cerebral
 CC vascular diseases, venous thromboembolism disease, coronary diseases,
 CC and metastatic cancers. The antibodies of the invention only causes a
 CC transient decrease in platelet counts, platelet aggregation, and/or
 CC platelet activation and so have some advantages over prior art
 CC methods. The present sequence represents a protein sequence used to
 CC create the antibodies of the invention.
 CC
 XX
 SQ Sequence 339 AA;
 Query Match 100.0%; Score 1786; DB 24; Length 339;
 Best Local Similarity 100.0%; Pred. No. 6.2e-141;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSPSPFALFCLGLGCRVPAQSGPLPKPSLQALPSLSLVPLEKPTLRGCGPPGVLYRLF 60
 DB 1 MSPSPFALFCLGLGCRVPAQSGPLPKPSLQALPSLSLVPLEKPTLRGCGPPGVLYRLF 60

QY 61 KLSSTRYQDQAVLFIIPAKKRSLAGRYCSYQNGSLMSLPSCQLELVATGVFAKPSLSAQF 120
 |||||
 CB 61 KLSSTRYQDQAVLFIIPAKKRSLAGRYCSYQNGSLMSLPSCQLELVATGVFAKPSLSAQF 120
 QY 121 GPAVSSGGDVTLQCCQTRVGFDDQALYKESDPAPYKKNPERWRASFFIITVTAHSGTYRC 180
 |||||
 Db 121 GPAVSSGGDVTLQCCQTRVGFDDQALYKESDPAPYKKNPERWRASFFIITVTAHSGTYRC 180
 QY 181 YSFSSRDPLWASDPLLELVVTGTSVTFPSRUPTEPPSSVAEFSSEATAELTWSFTNKVFT 240
 |||||
 Db 181 YSFSSRDPLWASDPLLELVVTGTSVTFPSRUPTEPPSSVAEFSSEATAELTWSFTNKVFT 240
 QY 241 TETSRISITTSPEKSDSPAGPARQYTKGNLVKICLGAVALITLILAGFLAEDWHSRKRLEH 300
 |||||
 Db 241 TETSRISITTSPEKSDSPAGPARQYTKGNLVKICLGAVALITLILAGFLAEDWHSRKRLEH 300
 QY 301 RGRAVQRPPLPPLPQTRKSHGGQDGGRCQDVHSRGJCS 339
 |||||
 Db 301 RGRAVQRPPLPPLPQTRKSHGGQDGGRCQDVHSRGJCS 339

RESULT 3

AAB61273
 ID AAB61273 standard; Protein; 339 AA.

AC AAB61273;

XX 04-APR-2001 (first entry)

DE Human TANGO 268-related protein #1.

XX Human; TANGO 268; cardiact; cerebroprotective; cyrostatic; anticoagulant;
 KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
 KW platelet membrane glycoprotein receptor; bleeding disorder;
 KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
 KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
 KW cancer.

OS Homo sapiens.

PN WO200100810-A1.

PD 04-JAN-2001.

PE 30-JUN-2000; 2000MO-US-8152.

PR 30-JUN-1999; 99US-0345468.

PR 06-DEC-1999; 99US-0454824.

PR 14-FEB-2000; 2000US-0503387.

PA (MILL-) MILLENNIUM PHARM INC.

PI Busfield SJ, Villalal J, Jandrot-Perrus M, Vainchenker W, Gill DS;

PI Qian MD, Kingsbury G;

XX KPI; 2001-060877/09.

XX N-PSDB; AAF29484.

XX New genes encoding human platelet-expressed collagen receptor;

XX glycoprotein VI, and its modulators, useful for preventing, treating

XX immunological disorders -

XX The present sequence is given in a specification relating to an isolated

XX nucleic acid molecule encoding a platelet membrane glycoprotein receptor

XX glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides

XX and polypeptides and their modulators, e.g. antisense nucleic acids,

XX ribozymes and antibodies, are useful for preventing, treating and

XX diagnosing disorders associated with aberrant expression or activity of

XX GPVI. These disorders include bleeding disorders

XX (e.g. thrombocytopenia), blood vessel injury, thrombotic disorders

CC (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
 CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
 CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
 CC infarction), immunological diseases (e.g. platelet disorder) and
 CC embryonic liver disorders. Preferably they are used to prevent acute
 CC cardiac ischaemia following angioplasty and metastatic cancers,
 CC especially of the colon and liver.

XX Sequence 339 AA;

Query Match 99.8%; Score 1782; DB 22; Length 339;

Best Local Similarity 99.7%; Pred. No. 1.3e-140;

Matches 339; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY : MSPFTALFCLGICLGRVPAQSGPLPKPSLQALPSSLVPLKPYTLKQGPFGVDYKLE 60
 |||||
 Db : MSPFTALFCLGICLGRVPAQSGPLPKPSLQALPSSLVPLKPYTLKQGPFGVDYKLE 60
 QY 61 KLSSTRYQDQAVLFIIPAKKRSLAGRYCSYQNGSLMSLPSCQLELVATGVFAKPSLSAQF 120
 |||||
 Db 61 KLSSTRYQDQAVLFIIPAKKRSLAGRYCSYQNGSLMSLPSCQLELVATGVFAKPSLSAQF 120
 QY 121 GPAVSSGGDVTLQCCQTRVGFDDQALYKESDPAPYKKNPERWRASFFIITVTAHSGTYRC 180
 |||||
 Db 121 GPAVSSGGDVTLQCCQTRVGFDDQALYKESDPAPYKKNPERWRASFFIITVTAHSGTYRC 180
 QY 181 YSFSSRDPLWASDPLLELVVTGTSVTFPSRUPTEPPSSVAEFSSEATAELTWSFTNKVFT 240
 |||||
 Db 181 YSFSSRDPLWASDPLLELVVTGTSVTFPSRUPTEPPSSVAEFSSEATAELTWSFTNKVFT 240
 QY 241 TETSRISITTSPEKSDSPAGPARQYTKGNLVKICLGAVALITLILAGFLAEDWHSRKRLEH 300
 |||||
 Db 241 TETSRISITTSPEKSDSPAGPARQYTKGNLVKICLGAVALITLILAGFLAEDWHSRKRLEH 300
 QY 301 RGRAVQRPPLPPLPQTRKSHGGQDGGRCQDVHSRGJCS 339
 |||||
 Db 301 RGRAVQRPPLPPLPQTRKSHGGQDGGRCQDVHSRGJCS 339

RESULT 4

AAB61274
 ID AAB61274 standard; Protein; 339 AA.

AC AAB61274;

DT 04-APR-2001 (first entry)

DE Human TANGO 268-related protein #2.

XX Human; TANGO 268; cardiact; cerebroprotective; cyrostatic; anticoagulant;
 KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
 KW platelet membrane glycoprotein receptor; bleeding disorder;
 KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
 KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
 KW cancer.

OS Homo sapiens.

PN WO200100810-A1.

PD 04-JAN-2001.

PE 30-JUN-2000; 2000MO-US-8152.

PR 30-JUN-1999; 99US-0345468.

PR 06-DEC-1999; 99US-0454824.

PR 14-FEB-2000; 2000US-0503387.

PA (MILL-) MILLENNIUM PHARM INC.

PI Busfield SJ, Villalal J, Jandrot-Perrus M, Vainchenker W, Gill DS;

PI Qian MD, Kingsbury G;

XX KPI; 2001-060877/09.

XX N-PSDB; AAF29484.

XX New genes encoding human platelet-expressed collagen receptor;

XX glycoprotein VI, and its modulators, useful for preventing, treating

XX immunological disorders -

XX The present sequence is given in a specification relating to an isolated

XX nucleic acid molecule encoding a platelet membrane glycoprotein receptor

XX glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides

XX and polypeptides and their modulators, e.g. antisense nucleic acids,

XX ribozymes and antibodies, are useful for preventing, treating and

XX diagnosing disorders associated with aberrant expression or activity of

XX GPVI. These disorders include bleeding disorders

XX (e.g. thrombocytopenia), blood vessel injury, thrombotic disorders

DR WP1: 2001-080877/09.
 DR N-PSDB: AAF29485.
 XX
 PT New genes encoding human platelet-expressed collagen receptor,
 PT glycoprotein VI, and its modulators, useful for preventing, treating
 PT and diagnosing hemorrhagic disorders, thrombotic diseases and
 PT immunological disorders -
 XX
 PS Disclosure: Page 214-215; 227pp; English.
 XX
 CC The present sequence is given in a specification relating to an isolated
 CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
 CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
 CC and polypeptides and their modulators, e.g. antisense nucleic acids,
 CC ribozymes and antibodies, are useful for preventing, treating and
 CC diagnosing disorders associated with aberrant expression or activity of
 CC GPVI. These disorders include bleeding disorders
 CC (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
 CC (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
 CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
 CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
 CC infarction), immunological diseases (e.g. platelet disorder) and
 CC embryonic liver disorders. Preferably they are used to prevent acute
 CC cardiac ischaemia following angioplasty and metastatic cancers.
 CC especially of the colon and liver.
 XX
 SQ Sequence 339 AA;
 Query Match 99.8%; Score 1782; DB 22; Length 339;
 Best Local Similarity 99.7%; Pred. No. 1,36-140;
 Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSPPTALFCLGCLGRVPAQSGPLPKPSLQALPSSLVPLPEKFTLRCCGPGVDYRL 60
 DB 1 MSPPTALFCLGCLGRVPAQSGPLPKPSLQALPSSLVPLPEKFTLRCCGPGVDYRL 60
 QY 61 KSSSRVQDQAVLFIPAKKRSIAGRYRCSYQNGSLMSLPDQELVATGVFAKPSLSAQ 120
 DB 61 KSSSRVQDQAVLFIPAKKRSIAGRYRCSYQNGSLMSLPDQELVATGVFAKPSLSAQ 120
 QY 121 GPAVSSGGDVTDQCOTRYGFDQFALYKESDPAPYKNPERWYRASFPITVTAHSGTYR 180
 DB 121 GPAVSSGGDVTDQCOTRYGFDQFALYKESDPAPYKNPERWYRASFPITVTAHSGTYR 180
 QY 181 YSFSSRDPLYLMSAPSDPELVWTGTSVTPSRLPTEPPSSVAEFSBATAELTVSFNKVFT 240
 DB 181 YSFSSRDPLYLMSAPSDPELVWTGTSVTPSRLPTEPPSSVAEFSBATAELTVSFNKVFT 240
 QY 241 TETSRITTSFKESDSPAGPAROYTKGNLVRIICGAVILILAGFLAEDWHSRRKRLRH 300
 DB 241 TETSRITTSFKESDSPAGPAROYTKGNLVRIICGAVILILAGFLAEDWHSRRKRLRH 300
 QY 301 RGRAVGRPLPLPLPQTRKSHGQDGGRODVHSRGLCS 339
 DB 301 RGRAVGRPLPLPLPQTRKSHGQDGGRODVHSRGLCS 339
 RESULT 3
 AAB61275
 ID AAB61275 standard; Protein; 339 AA.
 XX
 AC AAB61275;
 XX
 DT 04-APR-2001 (first entry)
 XX
 DE Human TANGO 268-related protein #3.
 XX
 KW Human; TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;
 KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
 KW platelet membrane glycoprotein receptor; bleeding disorder;
 KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
 KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
 KW cancer.

XX
 OS Homo sapiens.
 XX
 PR W0200100810-A1.
 XX
 PD 04-JAN-2001.
 XX
 PF 30-DEC-2000; 2000WO-US18152.
 XX
 PR 30-DEC-1999; 99US-0345468.
 PR 06-DEC-1999; 99US-0454824.
 PR 14-FEB-2000; 2000US-0503387.
 XX
 PA (WILL-) MILLENNIUM PHARM INC.
 XX
 PI Busfield SC, Villela J, Jandrot-Perrus W, Vainchencker W, Gill DS,
 PI Qian XC, Kingsbury G;
 XX
 DR N-PSDB: AAF29485.
 DR WP1: 2001-080877/09.
 XX
 PT New genes encoding human platelet-expressed collagen receptor,
 PT glycoprotein VI, and its modulators, useful for preventing, treating
 PT and diagnosing hemorrhagic disorders, thrombotic diseases and
 PT immunological disorders -
 XX
 PS Disclosure: Page 216; 227pp; English.
 XX
 CC The present sequence is given in a specification relating to an isolated
 CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
 CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
 CC and polypeptides and their modulators, e.g. antisense nucleic acids,
 CC ribozymes and antibodies, are useful for preventing, treating and
 CC diagnosing disorders associated with aberrant expression or activity of
 CC GPVI. These disorders include bleeding disorders
 CC (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
 CC (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
 CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
 CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
 CC infarction), immunological diseases (e.g. platelet disorder) and
 CC embryonic liver disorders. Preferably they are used to prevent acute
 CC cardiac ischaemia following angioplasty and metastatic cancers,
 CC especially of the colon and liver.
 XX
 SQ Sequence 339 AA;
 Query Match 99.8%; Score 1782; DB 22; Length 339;
 Best Local Similarity 99.7%; Pred. No. 1,36-140;
 Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSPPTALFCLGCLGRVPAQSGPLPKPSLQALPSSLVPLPEKFTLRCCGPGVDYRL 60
 DB 1 MSPPTALFCLGCLGRVPAQSGPLPKPSLQALPSSLVPLPEKFTLRCCGPGVDYRL 60
 QY 61 KSSSRVQDQAVLFIPAKKRSIAGRYRCSYQNGSLMSLPDQELVATGVFAKPSLSAQ 120
 DB 61 KSSSRVQDQAVLFIPAKKRSIAGRYRCSYQNGSLMSLPDQELVATGVFAKPSLSAQ 120
 QY 121 GPAVSSGGDVTDQCOTRYGFDQFALYKESDPAPYKNPERWYRASFPITVTAHSGTYR 180
 DB 121 GPAVSSGGDVTDQCOTRYGFDQFALYKESDPAPYKNPERWYRASFPITVTAHSGTYR 180
 QY 181 YSFSSRDPLYLMSAPSDPELVWTGTSVTPSRLPTEPPSSVAEFSBATAELTVSFNKVFT 240
 DB 181 YSFSSRDPLYLMSAPSDPELVWTGTSVTPSRLPTEPPSSVAEFSBATAELTVSFNKVFT 240
 QY 241 TETSRITTSFKESDSPAGPAROYTKGNLVRIICGAVILILAGFLAEDWHSRRKRLRH 300
 DB 241 TETSRITTSFKESDSPAGPAROYTKGNLVRIICGAVILILAGFLAEDWHSRRKRLRH 300
 QY 301 RGRAVGRPLPLPLPQTRKSHGQDGGRODVHSRGLCS 339
 DB 301 RGRAVGRPLPLPLPQTRKSHGQDGGRODVHSRGLCS 339

RESULT 6
AAB61276
ID AAB61276 standard; Protein; 339 AA;
XX
AC AAB61276;
XX
DT 04-APR-2001 (first entry)
XX
DE Human TANGO 268-related protein #1.
XX
KW Human; TANGO 268; cardiant; cerebroprotective; cytoprotect; anticoagulant;
KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
KW platelet membrane glycoprotein receptor; bleeding disorder;
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
KW cancer.
XX
OS Homo sapiens.
XX
FN WO200100810-A1.
XX
PD 04-JAN-2002.
XX
PE 30-JUN-2000; 2000WO-US18152.
XX
PR 30-JUN-1999; 99US-0345468.
PR 26-DEC-1999; 99US-0454824.
PR 14-FEB-2000; 2000US-0503387.
XX
PA (WILL-) MILLENNIUM PHARM INC.
XX
PI Busfield SJ, Vilellei C, Jandrot-Ferrus M, Vainchencker W, Gill DS;
PI Qian XE, Kingsbury G;
XX
DR WPI; 2001-080877/09.
DR N-PSDB; AAF29487.
XX
PT New genes encoding human platelet-expressed collagen receptor,
PT glycoprotein VI, and its modulators, useful for preventing, treating
PT and diagnosing hemorrhagic disorders, thrombotic diseases and
PT immunological disorders.
XX
PS Disclosure; Page 217; 227pp; English.
XX
CC The present sequence is given in a specification relating to an isolated
CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
CC and polypeptides and their modulators, e.g. antisense nucleic acids,
CC ribozymes and antibodies, are useful for preventing, treating and
CC diagnosing disorders associated with aberrant expression or activity of
CC GPVI. These disorders include bleeding disorders
CC (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
CC (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
CC infarction), immunological diseases (e.g. platelet disorder) and
CC embryonic liver disorders. Preferably they are used to prevent acute
CC cardiac ischaemia following angioplasty and metastatic cancers.
XX
SQ Sequence 339 AA;
XX
Query Match 99.8%; Score 1732; DS 22; Length 339;
Best Local Similarity 99.7%; Pred. No. 13e-140;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSPPPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSCLVPLEKPYTLRCCGPPGVLYRL 60
Db 1 MSPPPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSCLVPLEKPYTLRCCGPPGVLYRL 60
QY 61 KLSSSRVQDQAVLFPAKMSLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKRSLSAQP 120

RESULT 7
AABU1239
ID AABU1239 standard; Protein; 339 AA.
XX
AC AABU1239;
XX
DT 06-FEB-2003 (first entry)
XX
DE Glycoprotein VI associated protein sequence #1.
XX
KW Human; mouse; variable heavy; VI; antigen; cancer;
KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;
KW TANGO 268; extracellular matrix; collagen; platelet release;
KW proliferation; migration; embryogenesis; inflammation; thrombosis;
KW degeneration; thrombocytopaenia; antibody; thrombotic disorder;
KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
KW cardiovascular disease; angina pectoris; myocardial infarction;
KW coronary restenosis; atherosclerosis; immunological disorder;
KW developmental disorder; embryonic disorder; liver disorder;
KW cerebral vascular disease; venous thromboembolism disease.
XX
OS Homo sapiens.
XX
FN WO200280968-A1.
XX
PD 17-OCT-2002.
XX
PE 09-APR-2002; 2002WO-US11122.
XX
PR 09-APR-2002; 2001US-0829495.
XX
PA (WILL-) MILLENNIUM PHARM INC.
XX
PI Busfield SJ, Vilellei C, Jandrot-Ferrus M, Vainchencker W, Gill DS;
PI Qian XE, Kingsbury G;
XX
DR WPI; 2003-058477/05.
XX
PT Novel substantially purified antibody immunospecifically binding to
PT TANGO 268 antigen, useful for treating bleeding disorders such as
PT thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis
XX
PS Disclosure; Page 222-223; 236pp; English.
XX
CC This invention relates to a novel purified antibody comprising a
CC variable heavy (VH) complementarity determining region (CDR1, VH CDR2
CC or VH CDR3; or variable light (VL) CDR1, VL CDR2 or VL CDR3, and
CC immunospecifically binding to a TANGO 268 (also referred as glycoprotein
CC VI (GPVI)) antigen. The antibodies of the invention act to decrease or
CC block TANGO 268 binding to extracellular matrix components, or as a
CC collagen or platelet release and aggregation blocker. The antibodies of

CC The invention are useful for modulating proliferation, migration,
CC morphology, differentiation and/or function of megakaryocytes and
CC platelets, including during development e.g. embryogenesis, modulating
CC leukocyte-platelet and platelet-endothelium interactions in
CC inflammation and/or thrombosis, and modulating platelet aggregation and
CC degranulation. They are also useful for modulating disorders associated
CC with abnormal or aberrant megakaryocyte and/or platelet proliferation,
CC migration, morphology, differentiation and/or function, e.g. bleeding
CC disorders such as thrombocytopenia. Other diseases which may be
CC modulated by these antibodies are thrombotic disorders, cerebral
CC vascular diseases (e.g. stroke and ischaemia) venous thromboembolism
CC diseases (e.g. diseases involving leg swelling, pain and ulceration,
CC pulmonary embolism, etc); coronary diseases (e.g. cardiovascular
CC diseases including angina pectoris, myocardial infarction, coronary
CC stenosis, atherosclerosis, etc); immunological disorders,
CC developmental disorders, embryonic disorders, liver disorders, cerebral
CC vascular diseases, venous thromboembolism disease, coronary diseases,
CC and metastatic cancers. The antibodies of the invention only causes a
CC transient decrease in platelet counts, platelet aggregation, and/or
CC platelet activation and so have some advantages over prior art
CC methods. The present sequence represents a protein sequence used to
CC create the antibodies of the invention.

Sequence 339 AA;

Query Match	99.84%	Score 17821	DE 24	Length 339
Best Local Similarity	99.78%	Pred. No. 136140		
Matches 339	Conservative	0	Mismatches 1	Indels 0

```

0Y 1 XSFSTFALFCLGLCLGCRVFAOCSGLEKPSLCALPSLSLVLPLEKEPVLTRCCGPPGVCLNLE 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MSPSPFLAFCLGLCLGCRVFAOCSGLEKPSLCALPSLSLVLPLEKEPVLTRCCGPPGVCLNLE 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

0Y 61 KUSSSRVODQAVLFIPAKKRSJAGRYRCSYQNGSLMSLPDCLDLVATGVFAKESLSACP 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 KUSSSRVODQAVLFIPAKKRSJAGRYRCSYQNGSLMSLPDCLDLVATGVFAKESLSACP 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

0Y 121 GPVASSGSGEVLTCQCTRYGQDFALYKEGDPAPYKKNPBRWYRASFPILITVALHSGTYRC 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 GPVASSGSGEVLTCQCTRYGQDFALYKEGDPAPYKKNPBRWYRASFPILITVALHSGTYRC 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

0Y 161 YSFSSRDPEYLMASRPDLELVATGTSVTSRSLPTEPPSSVAEFSATAVELTYSPTNKWVF 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 161 YSFSSRDPEYLMASRPDLELVATGTSVTSRSLPTEPPSSVAEFSATAVELTYSPTNKWVF 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

0Y 241 TETSRSITTSPKESDSPAQGPAPRYVTKNLVRICGLAVTLLLAGFLAEDNWSRKKJLRH 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 TETSRSITTSPKESDSPAQGPAPRYVTKNLVRICGLAVTLLLAGFLAEDNWSRKKJLRH 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

0Y 301 RGPVAVQREPLFLPPLPQCTRKSHGGQCGGRQCVHRSKQLCS 339
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 RGPVAVQREPLFLPPLPQCTRKSHGGQCGGRQCVHRSKQLCS 339
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT

AB011240
ID AB011240 standard; Protein; 339 AA

AC ABU11240;

DT: 06-FEB-2003 (first entry)

DE Glycoprotein VI associated protein sequence #2

KM Human; mouse; variable heavy; VH; antigen; cancer;
KM complementarity determining region; TANGO 265; glycoprotein VI; GPVI
KM TANGO 268; extracellular matrix; collagen; platelet release;
KM proliferation; migration; embryogenesis; inflammation; thrombosis;
KM degradation; thrombocytopaenia; antibody; thrombotic disorder;
KM cerebral vascular disease; stroke; ischaemia; venous thromboembolism
KM leg swelling; pain; ulceration; pulmonary embolism; coronary disease
KM cardiovascular disease; angina pectoris; myocardial infarction;
KM coronary stenosis; atherosclerosis; immunological disorder;

KM developmental disorder; embryonic disorder; liver disorder;
 cerebral vascular disease; venous thromboembolism disease.

05 Homo sapiens

WC200280968-A1

FD 37-0CT-2002

PF 09-APR-2002; 2002WO-JS11122.

PR 09-APR-2001; 2001US-0829455.

PA (MILL-) VILLENIC PHARM INC.

PI Busfield SJ, Wilneval T, Jandrot-Perrus M, Vainchercker W, Gill DS

XX

Novel, substantially purified antibody immunospecifically binding to TANGC 268 antigen, useful for treating bleeding disorders such as thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis

PS Disclosure; Page 223-224; 236pp; English.

CC This invention relates to a novel purified antibody comprising a
CC variable heavy (VH) complementarity determining region (CDR1, VH CDR2
CC or VH CDR3; or variable light (VL) CDR1, VL CDR2 or VL CDR3, and
CC immunospecifically binding to a TANGO 268 (also referred as glycoprotein
CC VI (GPIIb)) antigen. The antibodies of the invention act to decrease or
CC block TANGO 268 binding to extracellular matrix components, or as a
CC collagen or platelet release and aggregation blocker. The antibodies of
CC the invention are useful for modulating proliferation, migration,
CC morphology, differentiation and/or function of megakaryocytes and
CC platelets, including during development e.g. embryogenesis, modulating
CC leukocyte-platelet and platelet-endothelium interactions in
CC inflammation and/or thrombosis, and modulating platelet aggregation and
CC degradation. They are also useful for modulating disorders associated
CC with abnormal or aberrant megakaryocyte and/or platelet proliferation,
CC migration, morphology, differentiation and/or function, e.g. bleeding
CC disorders such as thrombocytopaenia. Other diseases which may be
CC modulated by these antibodies are thrombotic disorders, cerebral
CC vascular diseases (e.g. stroke and ischaemia) venous thromboembolism
CC diseases (e.g. diseases involving leg swelling, pain and ulceration,
CC pulmonary embolism, etc); coronary diseases (e.g. cardiovascular
CC diseases including angina pectoris, myocardial infarction, coronary
CC stenosis, atherosclerosis, etc); immunological disorders,
CC developmental disorders, embryonic disorders, liver disorders, cerebral
CC vascular diseases, venous thromboembolism disease, coronary diseases,
CC and metastatic cancers. The antibodies of the invention only causes a
CC transient decrease in platelet counts, platelet aggregation, and/or
CC platelet activation and so have some advantages over prior art
CC methods. The present sequence represents a protein sequence used to
CC create the antibodies of the invention.

Sequence 339 AA;

Query March	99.8%	Score 1782;	DS 24;	Length 339;
Best Local Similarity	99.7%	Pred. No. 136-140;		
Matches 338; Conservative	0	Mismatches 1;	Indels 0;	Gaps 0;

QY 1 NSPSPTALFCLGLCGRVPAQSGPLPKPSLQALPSSLVPLEKPYLTLCQSGPEGVDDLYRLE 60
DB 1 NSPSPTALFCLGLCGRVPAQSGPLPKPSLQALPSSLVPLEKPYLTLCQSGPEGVDDLYRLE 60
QY 61 KLSSTRYQDQAVLFIFAMKRSLAGRYRCSYQNGSLSLSPDSQELVATGVFAKPSLSAQP 120
DB 61 KLSSTRYQDQAVLFIFAMKRSLAGRYRCSYQNGSLSLSPDSQELVATGVFAKPSLSAQP 120
QY :21 GPVSSGGDVTLLQCCSTRYGFQDQALYKEGDFAPYKPKERWYRASFPIITVTAHSGTYRC 180

Db 121 GPAVSSGGVTLQCCTRYGFDQFALYKSGDFAPYKPERWYRASPEIITVTAHSGTYRC 180
QY 161 YSFSSRDPLYMSAPSDPELVVTGTSVTPSRLLPTEPPSSVAEPSEATAELTVSGFTNKVFT 240
Cc 161 YSFSSRDPLYMSAPSDPELVVTGTSVTPSRLLPTEPPSSVAEPSEATAELTVSGFTNKVFT 240
Cc 241 TETSRITTSPEKESDSPAAGPARQVYTKGNLVRIICGAVILIIILAGFLAEDWHSRKRRLRH 300
Cc 241 TETSRITTSPEKESDSPAAGPARQVYTKGNLVRIICGAVILIIILAGFLAEDWHSRKRRLRH 300
QY 301 RGRAVGRPLPLPPLPQTRKSHGQDGRQDVHSRGLCS 339
Cc 301 RGRAVGRPLPLPPLPQTRKSHGQDGRQDVHSRGLCS 339
Db 301 RGRAVGRPLPLPPLPQTRKSHGQDGRQDVHSRGLCS 339
RESULT 9
ABU11241
ID ABU11241 standard; Protein; 339 AA.
XX
AC ABU11241;
XX
DT 06-FEB-2003 (first entry)
XX
DE Glycoprotein VI associated protein sequence #3.
XX
KW Human; mouse; variable heavy; VH; antigen; cancer;
KW complementarity determining region; TANGO 268; glycoprotein VI; GPII;
KW TANGO 268; extracellular matrix; collagen; platelet release;
KW proliferation; migration; embryogenesis; inflammation; thrombosis;
KW degeneration; thrombocytopenia; antibody; thrombotic disorder;
KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
KW cardiovascular disease; angina pectoris; myocardial infarction;
KW coronary restenosis; atherosclerosis; immunological disorder;
KW developmental disorder; embryonic disorder; liver disorder;
KW cerebral vascular disease; venous thromboembolism disease.
XX
OS Homo sapiens.
XX
PN MO200280968-A1.
XX
PD 17-OCT-2002.
XX
PF 09-APR-2002; 2002MO-US11122.
XX
PR 09-APR-2002; 2001US-0823495.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Busfield SJ, Villevat C, Jandrot-Perrus M, Vainchencker W, Gill DS;
PI Qian DX, Kingsbury G;
XX
DR WPI; 2003-058477/05.
XX
PT Novel, substantially purified antibody immunospecifically binding to
PT TANGO 268 antigen, useful for treating bleeding disorders such as
PT thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis
XX
PS Disclosure; Page 224-225; 236pp; English.
XX
Cc This invention relates to a novel purified antibody comprising a
Cc variable heavy (VH) complementarity determining region (CDR1, VH CDR2
Cc or VH CDR3; or variable light (VL) CDR1, VL CDR2 or VL CDR3, and
Cc immunospecifically binding to a TANGO 268 (also referred as glycoprotein
Cc VI (GPII)) antigen. The antibodies of the invention act to decrease or
Cc block TANGO 268 binding to extracellular matrix components, or as a
Cc collagen or platelet release and aggregation blocker. The antibodies of
Cc the invention are useful for modulating proliferation, migration,
Cc morphology, differentiation and/or function of megakaryocytes and
Cc platelets, including during development e.g. embryogenesis, modulating
Cc leukocyte-platelet and platelet-endothelium interactions in
Cc inflammation and/or thrombosis, and modulating platelet aggregation and

Cc degeneration. They are also useful for modulating disorders associated
Cc with abnormal or aberrant megakaryocyte and/or platelet proliferation,
Cc migration, morphology, differentiation and/or function, e.g. bleeding
Cc disorders such as thrombocytopenia. Other diseases which may be
Cc modulated by these antibodies are thrombotic disorders, cerebral
Cc vascular diseases (e.g. stroke and ischaemia) venous thromboembolism
Cc diseases (e.g. diseases involving leg swelling, pain and ulceration,
Cc pulmonary embolism, etc); coronary diseases (e.g. cardiovascular
Cc diseases including angina pectoris, myocardial infarction, coronary
Cc restenosis, atherosclerosis, etc); immunological disorders,
Cc developmental disorders, embryonic disorders, liver disorders, cerebral
Cc vascular diseases, venous thromboembolism disease, coronary diseases,
Cc and metastatic cancers. The antibodies of the invention only causes a
Cc transient decrease in platelet counts, platelet aggregation, and/or
Cc platelet activation and so have some advantages over prior art
Cc methods. The present sequence represents a protein sequence used to
Cc create the antibodies of the invention.
XX
SQ Sequence 339 AA;
XX
Query Match 99.8%; Score 1782; DB 24; Length 339;
Best Local Similarity 99.7%; Pred. No. 1,36-140;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSPSPALFCGLGCRVPAQSGPLPKPSLQAPSLVPLEKPYTRCGGPPGVLYRSE 60
Db 1 MSPSPALFCGLGCRVPAQSGPLPKPSLQAPSLVPLEKPYTRCGGPPGVLYRLE 60
QY 61 KLSSSRYQDAVLFIPAKKSLAGRYRCSYQNGSWSLPSDQLEVAAGVFAKPSUSAP 120
Db 61 KLSSSRYQDAVLFIPAKKSLAGRYRCSYQNGSWSLPSDQLEVAAGVFAKPSUSAP 120
QY 121 GPAVSSGGVTLQCCTRYGFDQFALYKSGDFAPYKPERWYRASPEIITVTAHSGTYRC 180
Db 121 GPAVSSGGVTLQCCTRYGFDQFALYKSGDFAPYKPERWYRASPEIITVTAHSGTYRC 180
QY 181 YSFSSRDPLYMSAPSDPELVVTGTSVTPSRLLPTEPPSSVAEPSEATAELTVSGFTNKVFT 240
Db 181 YSFSSRDPLYMSAPSDPELVVTGTSVTPSRLLPTEPPSSVAEPSEATAELTVSGFTNKVFT 240
QY 241 TETSRITTSPEKESDSPAAGPARQVYTKGNLVRIICGAVILIIILAGFLAEDWHSRKRRLRH 300
Db 241 TETSRITTSPEKESDSPAAGPARQVYTKGNLVRIICGAVILIIILAGFLAEDWHSRKRRLRH 300
QY 301 RGRAVGRPLPLPPLPQTRKSHGQDGRQDVHSRGLCS 339
Db 301 RGRAVGRPLPLPPLPQTRKSHGQDGRQDVHSRGLCS 339
RESULT 10
ABU11242
ID ABU11242 standard; Protein; 339 AA.
XX
XX
AC ABU11242;
XX
DT 06-FEB-2003 (first entry)
XX
DE Glycoprotein VI associated protein sequence #4.
XX
KW Human; mouse; variable heavy; VH; antigen; cancer;
KW complementarity determining region; TANGO 268; glycoprotein VI; GPII;
KW TANGO 268; extracellular matrix; collagen; platelet release;
KW proliferation; migration; embryogenesis; inflammation; thrombosis;
KW degeneration; thrombocytopenia; antibody; thrombotic disorder;
KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
KW cardiovascular disease; angina pectoris; myocardial infarction;
KW coronary restenosis; atherosclerosis; immunological disorder;
KW developmental disorder; embryonic disorder; liver disorder;
KW cerebral vascular disease; venous thromboembolism disease.
XX
OS Homo sapiens.
XX

EN WO200283968-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 09-APR-2002; 2002WO-0511122.
 XX
 PR 09-APR-2001; 2001US-0829495.
 XX
 PA (MILL.) MILLENNIUM PHARM INC.
 XX
 PI Busfield SJ, Villevall J, Candrot-Perrus M, Vainchencker W, Gill DS;
 PI Qian DM, Kingsbury G;
 XX
 XX WPI; 2003-058477/05.
 XX
 PT Novel substantially purified antibody immunospecifically binding to
 PT TANGC 268 antigen, useful for treating bleeding disorders such as
 PT thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis
 PT
 XX
 PS Disclosure; Page 226; 236pp; English.
 XX
 CC This invention relates to a novel purified antibody comprising a
 CC variable heavy (VH) complementarity determining region (CDR1, VH CDR2
 CC or VH CDR3; or variable light (VL) CDR1, VL CDR2 or VL CDR3, and
 CC immunospecifically binding to a TANGC 268 (also referred as glycoprotein
 CC VI (GPVI)) antigen. The antibodies of the invention act to decrease or
 CC block TANGC 268 binding to extracellular matrix components, or as a
 CC collagen or platelet release and aggregation blocker. The antibodies of
 CC the invention are useful for modulating proliferation, migration,
 CC morphology, differentiation and/or function of megakaryocytes and
 CC platelets, including during development e.g. embryogenesis, modulating
 CC leukocyte-platelet and platelet-endothelial interactions in
 CC inflammation and/or thrombosis, and modulating platelet aggregation and
 CC degradation. They are also useful for modulating platelet proliferation
 CC with abnormal or aberrant megakaryocyte and/or platelet proliferation,
 CC migration, morphology, differentiation and/or function, e.g. Platelet
 CC disorders such as thrombocytopenia. Other diseases which may be
 CC modulated by these antibodies are thrombotic disorders, cerebral
 CC vascular diseases (e.g. stroke and ischaemia), venous thromboembolism
 CC diseases (e.g. diseases involving leg swelling, pain and ulceration,
 CC pulmonary embolism, etc); coronary diseases (e.g. cardiovascular
 CC diseases including angina pectoris, myocardial infarction, coronary
 CC restenosis, atherosclerosis, etc); immunological disorders,
 CC developmental disorders, embryonic disorders, liver disorders, cerebral
 CC vascular diseases, venous thromboembolism disease, coronary diseases,
 CC and metastatic cancers. The antibodies of the invention only causes a
 CC transient decrease in platelet counts, platelet aggregation, and/or
 CC platelet activation and so have some advantages over prior art
 CC methods. The present sequence represents a protein sequence used to
 CC create the antibodies of the invention.
 CC
 XX
 SQ Sequence 339 AA;
 Query Match 99.8%; Score 1782; DB 24; Length 339;
 Best Local Similarity 99.7%; Pred. No. 1,38-140;
 Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSPSFALFCJGLGKRVPAQSGPSPKPSLQALPSSLVPLEKPYTRCGGPGVYRLRLE 60
 DB 1 MSPSFALFCJGLGKRVPAQSGPSPKPSLQALPSSLVPLEKPYTRCGGPGVYRLRLE 60
 QY 61 KJSSSRQDOAVLFIPAMKRSLAGRYRCSYQNGSLWSPSDQLELWATGVPAKRSUSACP 120
 DB 61 KJSSSRQDOAVLFIPAMKRSLAGRYRCSYQNGSLWSPSDQLELWATGVPAKRSUSACP 120
 QY 121 GPAVSSGGSDVTLQCCQTRYGFDQFALYKEGDPAPYKXPERWYRASPPIITVTAAHSGTYRC 180
 DB 121 GPAVSSGGSDVTLQCCQTRYGFDQFALYKEGDPAPYKXPERWYRASPPIITVTAAHSGTYRC 180
 QY 181 YSFSRRDPYLMASPDPLELVLTGIVTPSRLEPTEPSSVAEFSEATAELTWSFTNKVFT 240
 DB 181 YSFSRRDPYLMASPDPLELVLTGIVTPSRLEPTEPSSVAEFSEATAELTWSFTNKVFT 240

QY 241 TETSRSTTSPEKSDSPAGPARQYVTKCNLVRIQGLAVILLIAGFLAEQWHSRPRKLRH 300
 DB 241 TETSRSTTSPEKSDSPAGPARQYVTKCNLVRIQGLAVILLIAGFLAEQWHSRPRKLRH 300
 QY 301 RGRAVQRPPLPPLPQTRKSHGGQDGGGRQDVHSRGJCS 339
 DB 301 RGRAVQRPPLPPLPQTRKSHGGQDGGGRQDVHSRGJCS 339
 RESULT 11
 AAB31668
 ID AAB31668 standard; Protein: 339 AA.
 AC AAB31668;
 XX
 XX 30-APR-2001 (first entry)
 DE Amino acid sequence of a human protein having a hydrophobic domain.
 XX
 XX Human; hydrophobic protein; secretory protein; membrane protein; sepsis;
 XX tumour inhibition; immune deficiency; autoimmune disorder; anaemia; burn;
 XX infectious disease; cancer; ulcer; periodontal disease; coagulation;
 XX Parkinson's disease; fertility; immune response; thrombosis.
 OS Homo sapiens.
 PK WO200104297-A2.
 XX 18-JAN-2001.
 PF 16-JUN-2000; 2000MO-CF03942.
 XX 08-JUL-1999; 99JP-0194359.
 PA (SAGA) SAGAMI CHEM RES CENT.
 PA (PROT.) PROTEGENE INC.
 PI Kato S, Kimura T;
 DR WPI; 2001-103082/11.
 DR N-PSDB; AAF25158, AAF25168.
 XX
 PT Isolated human proteins and polynucleotides are used in research and
 PT have activities including cell proliferation/differentiation activity,
 PT immune stimulating activity and receptor/ligand activity -
 PS Claim 1: Page 88-90; 151pp; English.
 XX
 CC The present sequence represents a human protein with hydrophobic domains.
 CC The protein possesses a hydrophobic domain and so is a secretory protein
 CC or a membrane protein. The protein is used as an antigen to prepare
 CC antibodies. The polynucleotide sequence is useful as a source of probes
 CC for genetic diagnosis. It is also useful for producing the protein
 CC in large quantities and for gene therapy. The eukaryotic cells are used
 CC for detecting the receptors or ligands corresponding to the protein and
 CC for detecting small novel pharmaceuticals. The antibodies are also used
 CC for detection, quantification and purification of the proteins. Both the
 CC protein and polynucleotide may be used in research or as nutritional
 CC sources or supplements. The protein may have cytokine and cell
 CC proliferation/differentiation activity, immune stimulating or suppressing
 CC activity, hematopoiesis regulating activity, tissue growth activity,
 CC activity/inhibin activity, chemotactic/chemokinetic activity, hemostatic
 CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
 CC activity and tumour inhibition activity. It may therefore may be used to
 CC treat immune deficiencies resulting from autoimmune disorders or
 CC infectious diseases, cancer, sepsis, anaemias, burns and ulcers,
 CC periodontal disease, Parkinson's disease, induce fertility, improve
 CC immune response and enhance coagulation or inhibit thrombosis.
 SQ Sequence 339 AA;
 Query Match 99.8%; Score 1770; DB 22; Length 339;

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Best Local Similarity 99.1%; Pred. No. 1,3e-139;
Matches 336; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSPSPFALFCLGLCLGRVPAQSGPLPKPSLQALPSSLYPLEKPVTLRCGGPAGVDLYRLS 60
DQ 1 MSPSPFALFCLGLCLGRVPAQSGPLPKPSLQALPSSLYPLEKPVTLRCGGPAGVDLYRLS 60
QY 61 KLSSSRVQDQAVLFIPAMKSLAGRYRCSYQNGSLMSLPDQLELVATGVFAKPSLSAQP 120
DQ 61 KLSSSRVQDQAVLFIPAMKSLAGRYRCSYQNGSLMSLPDQLELVATGVFAKPSLSAQP 120
QY 121 GPAVSSGGDVTLQCCQTRYGFDQFALYKESDPAPYKNERWYRASFPILITVTAASGTYRC 180
DQ 121 GPAVSSGGDVTLQCCQTRYGFDQFALYKESDPAPYKNERWYRASFPILITVTAASGTYRC 180
QY 181 YSPSSRDYPLMSAPSDPLELVVTGTSVTPSRLLPTPEPSSVAEFSEATAEITVSTNKVFT 240
DQ 181 YSPSSRDYPLMSAPSDPLELVVTGTSVTPSRLLPTPEPSSVAEFSEATAEITVSTNKVFT 240
QY 241 TETSRITTSPEKESDSPAQAPQYVTKGNLVRIQGLAVILITLAGFLAEDWHSRRKRLRH 300
DQ 241 TETSRITTSPEKESDSPAQAPQYVTKGNLVRIQGLAVILITLAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVQRPPLPPLPPLPQTRKSHGGQDGGRCQVHSRGLCS 339
DQ 301 RGRAVQRPPLPPLPPLPQTRKSHGGQDGGRCQVHSRGLCS 339

RESULT 12
AAY72790 standard; Protein: 339 AA.
XX AC AAY72790;
XX DT 31-MAY-2001 (first entry)
XX DE Human platelet membrane glycoprotein VI (GPVI).
XX KW Human; platelet membrane glycoprotein VI; GPVI; thrombolytic; therapy;
XX KW vascular disease; thrombosis.
XX CS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 1..23
XX FT Protein /label= Signal_peptide
XX FT 24..339
XX FT /note= "Mature platelet membrane glycoprotein VI
XX FT (GPVI) protein"
XX FT Domain 24..263
XX FT /label= Extracellular_domain
XX FT Misc-difference 74
XX FT /note= "Encoded by TTC"
XX FT Misc-difference 100
XX FT /note= "Encoded by AAC"
XX FT Misc-difference 114
XX FT /note= "Encoded by CCC"
XX FT Misc-difference 166
XX FT /note= "Encoded by CCC"
XX PN WC000116321-A1.
XX PD 08-MAR-2001.
XX XX
XX PF 01-SEP-2000; 2000WC-US23975.
XX PR 01-SEP-1999; 99JUS-0152197.
XX PR 08-OCT-1999; 99JUS-0158251.
XX PA (SUKA : OTSUKA PHARM CO LTD.
XX PI Tandon N, Sun B, Nakamura T, Yamamoto N;
XX XX
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DR MPI; 2001-226691/23.
DR K-PSDB; AAD02855.
XX PT Anti-thrombotic medicament, comprising a polypeptide having the
XX FT extracellular domain of platelet membrane glycoprotein VI or its
XX FT variant, useful for treating a vascular disease and reducing platelet
XX FT activation.
XX PS Disclosure; Fig 3; 74pp; English.
XX XX
CC The present sequence is a human platelet membrane glycoprotein VI
CC (GPVI). The medicament comprising GPVI is useful for treating
CC vascular disease, and for reducing platelet activation which involves
CC contacting platelets with the medicament. The extracellular portion of
CC GPVI is used therapeutically to attenuate platelet activation and
CC aggregation and to treat thrombosis and other vascular diseases.
CC Antibodies generated against GPVI are used as research and
CC immunotherapeutic agents.
XX SQ Sequence 339 AA;
XX XX
Query Match 98.5%; Score 1759; DB 22; Length 339;
Best Local Similarity 99.1%; Pred. No. 1,3e-138;
Matches 336; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSPSPFALFCLGLCLGRVPAQSGPLPKPSLQALPSSLYPLEKPVTLRCGGPAGVDLYRLS 60
DQ 1 MSPSPFALFCLGLCLGRVPAQSGPLPKPSLQALPSSLYPLEKPVTLRCGGPAGVDLYRLS 60
QY 61 KLSSSRVQDQAVLFIPAMKSLAGRYRCSYQNGSLMSLPDQLELVATGVFAKPSLSAQP 120
DQ 61 KLSSSRVQDQAVLEIPAMKSLAGRYRCSYQNGSLMSLPDQLELVATGVFAKPSLSAQP 120
QY 121 GPAVSSGGDVTLQCCQTRYGFDQFALYKESDPAPYKNERWYRASFPILITVTAASGTYRC 180
DQ 121 GPAVSSGGDVTLQCCQTRYGFDQFALYKESDPAPYKNERWYRASFPILITVTAASGTYRC 180
QY 181 YSPSSRDYPLMSAPSDPLELVVTGTSVTPSRLLPTPEPSSVAEFSEATAEITVSTNKVFT 240
DQ 181 YSPSSRDYPLMSAPSDPLELVVTGTSVTPSRLLPTPEPSSVAEFSEATAEITVSTNKVFT 240
QY 241 TETSRITTSPEKESDSPAQAPQYVTKGNLVRIQGLAVILITLAGFLAEDWHSRRKRLRH 300
DQ 241 TETSRITTSPEKESDSPAQAPQYVTKGNLVRIQGLAVILITLAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVQRPPLPPLPPLPQTRKSHGGQDGGRCQVHSRGLCS 339
DQ 301 RGRAVQRPPLPPLPPLPQTRKSHGGQDGGRCQVHSRGLCS 339

RESULT 13
AAB61257
XX ID AAB61257 standard; Protein: 319 AA.
XX AC AAB61257;
XX DT 04-APR-2001 (first entry)
XX DE Mature human TANGO 268 protein.
XX KW Human; TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;
XX KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
XX KW platelet membrane glycoprotein receptor; bleeding disorder;
XX KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
XX KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
XX KW cancer.
XX CS Homo sapiens.
XX XX
XX PN WC0200100810-A1.
XX PD 04-JAN-2001.
XX XX
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PF 30-JUN-2000; 2000MC-US18152.
XX
PR 30-JUN-1999; 99US-0345468.
PR 06-DEC-1999; 99US-0454824.
PR 14-FEB-2000; 2000US-0503387.
XX
PA (WILL-) MILLENNIUM PHARM INC.
XX
PI Busfield SJ, Villetta J, Candrot-Perrus X, Vainchencker W, Gili D;
PI Qian MD, Kingsbury G;
XX
DR W21; 2001-080877/09.
XX
PT New genes encoding human platelet-expressed collagen receptor,
PT Glycoprotein VI, and its modulators, useful for preventing,
PT and diagnosing hemorrhagic disorders, thrombotic diseases and
PT immunological disorders -
XX
PS Disclosure; Fig 2; 227pp; English.

XX The present sequence is given in a specification relating to an isolated
XX nucleic acid molecule encoding a platelet membrane glycoprotein receptor
XX glycoprotein VI (GPVI), also called TACD 268. The GPVI polynucleotides
XX and polypeptides and their modulators, e.g. antisense nucleic acids,
XX ribozymes and antibodies, are useful for preventing, treating and
XX diagnosing disorders associated with aberrant expression or activity of
XX GPVI. These disorders include bleeding disorders
XX (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
XX (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
XX disorders, coronary artery and cerebral artery diseases (e.g. stroke and
XX ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
XX infarction), immunological diseases (e.g. platelet disorder) and
XX embryonic liver disorders. Preferably they are used to prevent acute
XX cardiac ischaemia following angioplasty and metastatic cancers,
XX especially of the colon and liver.

XX Sequence 319 AA;

Query Match 94.0%; Score 1678; DB 22; Length 319;
Best Local Similarity 100.0%; Pred. No. 6,1e-132;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 QSGFLPKPSQALPSSLYPLEKPYTLKCGPPGVLDYRLEKLSRRYQDQAVLFTAMKP 80
DB 1 QSGFLPKPSQALPSSLYPLEKPYTLKCGPPGVLDYRLEKLSRRYQDQAVLFTAMKP 80
QY 61 SIAGRYRCGYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGCVTLQCGTRYGF 140
DB 61 SIAGRYRCGYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGCVTLQCGTRYGF 120
QY 141 EQFALYKESGFAPYKPERMYRASFPITVTAAHSGTYRCYSFSSRDYPLWSAPSDLEL 200
DB 121 EQFALYKESGFAPYKPERMYRASFPITVTAAHSGTYRCYSFSSRDYPLWSAPSDLEL 180
QY 201 VVTGTSVTSRPLPTPEPSSVAEFSEATLTLVSFTNKVYTTETTSRSITTSKESDSAPGP 260
DB 181 VVTGTSVTSRPLPTPEPSSVAEFSEATLTLVSFTNKVYTTETTSRSITTSKESDSAPGP 240
QY 261 ARQYTTKGNLVRICTGAVILITLAGFLAEDWHSRRKRLRHGRAVQRPPLPLPQTRK 320
DB 241 ARQYTTKGNLVRICTGAVILITLAGFLAEDWHSRRKRLRHGRAVQRPPLPLPQTRK 300
QY 321 SHGGQDGGRODVHSRGLCS 339
DB 301 SHGGQDGGRODVHSRGLCS 319

RESULT 14
AAB49403
ID AAB49403 standard; Protein; 319 AA.
XX
AC AAB49403;
XX

QY 05-MAR-2001 (First entry)
XX
DE Human glycoprotein VI mature protein.
XX
XX Human; thrombolytic; cardiac; glycoprotein VI; GPVI;
XX platelet membrane glycoprotein; platelet activation;
XX platelet-collagen interaction; thrombotic disorder;
XX cardiovascular disorder.
XX
OS Homo sapiens.
XX
PN WO200065377-A1.
XX
PD 16-NOV-2000.
XX
PF 25-APR-2000; 2000WO-EP03683.
XX
PR 07-MAY-1999; 99EP-0139094.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Clemetson KJ;
XX
DR WPI; 2001-007394/01.
DR N-PSDB; AAC83980.

XX Recombinant human glycoprotein VI, useful for treating thrombotic,
PT cardiovascular diseases or platelet-collagen interactions -
XX
XX Claim 5; Fig 1; 27pp; English.

XX The present sequence is human glycoprotein VI (GPVI) mature protein. GPVI
XX is a platelet membrane glycoprotein which forms a complex together with
XX the Fc gamma common subunit, which is critical for platelet activation in
XX response to collagen. GPVI is useful as a screening tool for detecting
XX specific inhibitors of platelet-collagen interactions, and as a marker
XX for platelet age and platelet exposure to thrombotic and cardiovascular
XX disorders. GPVI is also useful for the manufacture of medicaments in the
XX therapeutic field of thrombotic and cardiovascular events, and disorders
XX related to platelet-collagen interactions.

XX Sequence 319 AA;

Query Match 94.0%; Score 1678; DB 22; Length 319;
Best Local Similarity 100.0%; Pred. No. 6,1e-132;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 QSGFLPKPSQALPSSLYPLEKPYTLKCGPPGVLDYRLEKLSRRYQDQAVLFTAMKP 80
DB 1 QSGFLPKPSQALPSSLYPLEKPYTLKCGPPGVLDYRLEKLSRRYQDQAVLFTAMKP 80
QY 61 SIAGRYRCGYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGCVTLQCGTRYGF 140
DB 61 SIAGRYRCGYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGCVTLQCGTRYGF 120
QY 141 EQFALYKESGFAPYKPERMYRASFPITVTAAHSGTYRCYSFSSRDYPLWSAPSDLEL 200
DB 121 EQFALYKESGFAPYKPERMYRASFPITVTAAHSGTYRCYSFSSRDYPLWSAPSDLEL 180
QY 201 VVTGTSVTSRPLPTPEPSSVAEFSEATLTLVSFTNKVYTTETTSRSITTSKESDSAPGP 260
DB 181 VVTGTSVTSRPLPTPEPSSVAEFSEATLTLVSFTNKVYTTETTSRSITTSKESDSAPGP 240
QY 261 ARQYTTKGNLVRICTGAVILITLAGFLAEDWHSRRKRLRHGRAVQRPPLPLPQTRK 320
DB 241 ARQYTTKGNLVRICTGAVILITLAGFLAEDWHSRRKRLRHGRAVQRPPLPLPQTRK 300
QY 321 SHGGQDGGRODVHSRGLCS 339
DB 301 SHGGQDGGRODVHSRGLCS 319

RESULT 15

ABU11223
 ID ABU11223 standard; Protein: 319 AA.
 XX
 AC ABU11223;
 XX
 DT 06-FEB-2003 (first entry)
 XX
 LE Human TANGO 268 mature protein.
 XX
 KW Human; mouse; variable heavy; VH; antigen; cancer;
 KW complementarity determining region; TANGO 268; glycoprotein VI; GPIIb;
 KW TANGO 268; extracellular matrix; collagen; platelet release;
 KW proliferation; migration; embryogenesis; inflammation; thrombosis;
 KW degradation; thrombocytopaenia; antibody; thrombotic disorder;
 KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
 KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
 KW cardiovascular disease; angina pectoris; myocardial infarction;
 KW coronary stenosis; atherosclerosis; immunological disorder;
 KW developmental disorder; embryonic disorder; liver disorder;
 KW cerebral vascular disease; venous thromboembolism disease.
 XX
 CS Homo sapiens.
 XX
 PN W0200250968-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 09-APR-2002; 2002WO-US11122.
 XX
 PR 09-APR-2002; 2001US-0829495.
 XX
 PA (WILL-) MILLENNIUM PHARM INC.
 XX
 FI Busfield SJ, Willevall J, Cardrol-Perrus M, Vainchercker W, Gill DS;
 PI Qian CM, Kingsbury G;
 XX
 DR WPI; 2003-056477/05.
 XX
 PT Novel substantially purified antibody immunospecifically binding to
 PT TANGO 268 antigen, useful for treating bleeding disorders such as
 PT thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis
 PT
 PS Disclosure; Page 2:1-212; 236pp; English.
 XX
 CC This invention relates to a novel purified antibody comprising a
 CC variable heavy (VH) complementarity determining region (CDR1, VH CDR2
 CC or VH CDR3; or variable light (VL) CDR1, VL CDR2 or VL CDR3, and
 CC immunospecifically binding to a TANGO 268 (also referred as glycoprotein
 CC VI (GPIIb)) antigen. The antibodies of the invention act to decrease or
 CC block TANGO 268 binding to extracellular matrix components, or as a
 CC collagen or platelet release and aggregation blocker. The antibodies of
 CC the invention are useful for modulating proliferation, migration,
 CC morphology, differentiation and/or function of megakaryocytes and
 CC platelets, including during development e.g. embryogenesis, modulating
 CC leukocyte-platelet and platelet-endothelium interactions in
 CC inflammation and/or thrombosis, and modulating platelet aggregation and
 CC degradation. They are also useful for modulating disorders associated
 CC with abnormal or aberrant megakaryocyte and/or platelet proliferation,
 CC migration, morphology, differentiation and/or function, e.g. bleeding
 CC disorders such as thrombocytopaenia. Other diseases which may be
 CC modulated by these antibodies are thrombotic disorders, cerebral
 CC vascular diseases (e.g. stroke and ischaemia) venous thromboembolism
 CC diseases (e.g. diseases involving leg swelling, pain and ulceration,
 CC pulmonary embolism, etc); coronary diseases (e.g. cardiovascular
 CC diseases including angina pectoris, myocardial infarction, coronary
 CC stenosis, atherosclerosis, etc); immunological disorders,
 CC developmental disorders, embryonic disorders, liver disorders, cerebral
 CC vascular diseases, venous thromboembolism disease, coronary diseases,
 CC and metastatic cancers. The antibodies of the invention only causes a
 CC transient decrease in platelet counts, platelet aggregation, and/or
 CC platelet activation and so have some advantages over prior art
 CC methods. The present sequence represents a protein sequence used to

CC create the antibodies of the invention.
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 SQ Sequence 319 AA;
 Query Match 94.0%; Score 1678; DB 24; Length 319;
 Best Local Similarity 100.0%; Pred. No. 6,1e-132;
 Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 1 QSGPLPKPSLQALPSSSLVPLEKPYTLRCQSPGVDLYRLEKLSRRYCCQAVLTPMKR 60
 61 SLAGRYRCSYQNGSLMSLPSDQLSLVATGVFAKPSLSAQPGFAVSSGSDVTLCCQRYGF 140
 61 SLAGRYRCSYQNGSLMSLPSDQLSLVATGVFAKPSLSAQPGFAVSSGSDVTLCCQRYGF 120
 241 EQFALYKESDPAPYKPKRWYRAAPPIITVTAHSGTYRCYSSSRPPYIWSAPSPLE 200
 121 EQFALYKESDPAPYKPKRWYRAAPPIITVTAHSGTYRCYSSSRPPYIWSAPSPLE 180
 201 VWTGTSVTPSRLPTSPSSVAERSAATLTVSGTNKVFTTETSRSITSPKESDPAGP 260
 161 VWTGTSVTPSRLPTSPSSVAERSAATLTVSGTNKVFTTETSRSITSPKESDPAGP 240
 261 ARQYITKGNLVRICTGAVIITLACFLAEDWGRKRLRHGRAYORFLPPLPDPQTRK 320
 241 ARQYITKGNLVRICTGAVIITLACFLAEDWGRKRLRHGRAYORFLPPLPDPQTRK 300
 321 SHGGQDGGROQDVHSGSGLCS 339
 301 SHGGQDGGROQDVHSGSGLCS 319

Search completed: October 23, 2003, 09:41:40
 Job time : 84 secs

GenCore version 5.1.6
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ON protein - protein search, using sw model

Run on: October 23, 2003, 09:41:49 ; Search time 71 Seconds

(without alignments)
799,566 Million cell updates/sec

Title: US-09-503-387-3

Perfect score: 1786

Sequence: 1 MSPSPALFCLGLGCRVPAAGSPGLPKPSLQALPSSLVPLEKPVITACOGPPGVLYRLR 60

Scoring table: BIOSUM62

Gapop 13.0 , Gapext 3.5

Searched: 629382 seqs, 167460630 residues

Total number of hits satisfying chosen parameters: 629382

Minimum DB seq length: 5
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PC1_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US0A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1786	100.0	339	9	US-09-832-312-3	Sequence 3, Appl 1
2	1786	100.0	339	15	US-10-157-031-367	Sequence 397, App
3	1782	99.8	339	9	US-09-832-312-34	Sequence 34, Appl 1
4	1782	99.8	339	9	US-09-832-312-36	Sequence 36, Appl 1
5	1782	99.8	339	9	US-09-832-312-38	Sequence 38, Appl 1
6	1782	99.8	339	9	US-09-832-312-40	Sequence 40, Appl 1
7	1759	98.5	339	12	US-10-446-826-5	Sequence 5, Appl 1
8	1678	94.0	319	9	US-09-832-312-5	Sequence 5, Appl 1
9	1304	73.0	249	9	US-09-832-312-9	Sequence 9, Appl 1
10	1304	73.0	369	12	US-10-446-826-37	Sequence 37, Appl 1
11	1122	62.8	313	9	US-09-832-312-16	Sequence 16, Appl 1
12	1122	62.8	313	9	US-09-832-312-46	Sequence 46, Appl 1
13	1118	62.6	313	9	US-09-832-312-42	Sequence 42, Appl 1
14	1118	62.6	313	9	US-09-832-312-44	Sequence 44, Appl 1
15	1118	62.6	313	9	US-09-832-312-46	Sequence 46, Appl 1

16	1080.5	60.5	292	9	US-09-832-312-18	Sequence 18, Appl 1
17	937	52.5	267	9	US-09-832-312-19	Sequence 19, Appl 1
18	498	27.9	447	10	US-09-870-759-50	Sequence 50, Appl 1
19	498	27.9	447	12	US-09-751-708A-50	Sequence 50, Appl 1
20	498	27.9	448	12	US-10-143-618-18	Sequence 18, Appl 1
21	498	27.9	448	15	US-10-139-662-18	Sequence 18, Appl 1
22	498	27.9	448	15	US-10-139-683-18	Sequence 18, Appl 1
23	497	27.5	447	11	US-09-978-418-36	Sequence 36, Appl 1
24	477	26.7	289	12	US-10-143-618-12	Sequence 12, Appl 1
25	477	26.7	289	15	US-10-139-662-12	Sequence 12, Appl 1
26	477	26.7	289	15	US-10-139-683-12	Sequence 12, Appl 1
27	457	25.6	632	12	US-10-114-153-92	Sequence 92, Appl 1
28	455	25.5	299	11	US-09-796-753-144	Sequence 144, Appl 1
29	455	25.5	299	15	US-10-139-662-30	Sequence 30, Appl 1
30	455	25.5	299	15	US-10-139-683-30	Sequence 30, Appl 1
31	454	25.4	631	9	US-09-832-312-12	Sequence 12, Appl 1
32	449	25.1	631	12	US-10-143-618-20	Sequence 20, Appl 1
33	449	25.1	631	15	US-10-139-662-20	Sequence 20, Appl 1
34	449	25.1	631	15	US-10-139-683-20	Sequence 20, Appl 1
35	441	24.7	466	10	US-09-944-807-12	Sequence 12, Appl 1
36	441	24.7	483	12	US-10-143-618-16	Sequence 16, Appl 1
37	441	24.7	483	15	US-10-139-662-16	Sequence 16, Appl 1
38	441	24.7	483	15	US-10-139-683-16	Sequence 16, Appl 1
39	439.5	24.6	489	12	US-10-143-618-14	Sequence 14, Appl 1
40	439.5	24.6	489	15	US-10-139-662-14	Sequence 14, Appl 1
41	439.5	24.6	489	15	US-10-139-683-14	Sequence 14, Appl 1
42	438	24.5	431	15	US-10-290-631-14	Sequence 14, Appl 1
43	438	24.5	431	15	US-10-290-631-20	Sequence 20, Appl 1
44	434	24.3	598	12	US-10-143-618-10	Sequence 10, Appl 1
45	434	24.3	598	15	US-10-139-662-10	Sequence 10, Appl 1

ALIGNMENTS

RESULT 1
US-09-832-312-3
Sequence 3, Application US/09832312
Patent No. US20010049829A1
GENERAL INFORMATION:
APPLICANT: Busfield et al.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-234
CURRENT APPLICATION NUMBER: US/09/832,312
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
US-09-832-312-3

Query Match 100.0%; Score 1786; DB 9; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-139;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MSPSPALFCLGLGCRVPAAGSPGLPKPSLQALPSSLVPLEKPVITACOGPPGVLYRLR 60
DB 1 MSPSPALFCLGLGCRVPAAGSPGLPKPSLQALPSSLVPLEKPVITACOGPPGVLYRLR 60
CY 61 KLSSRYQDAVLFIPAMKSLAGRYRCSYONGSLMSLPSCLELVATGVFAKPSLSAQP 120
DB 61 KLSSRYQDAVLFIPAMKSLAGRYRCSYONGSLMSLPSCLELVATGVFAKPSLSAQP 120

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QY 121 GPAVSSGGDVTLCCQTRYGFDQALYKEGDPAPYKKNPERWYKASFPITVTAAHSGTYRC 180
D 121 GPAVSSGGDVTLCCQTRYGFDQALYKEGDPAPYKKNPERWYKASFPITVTAAHSGTYRC 180
QY 181 YSFSSRDPLYLWSAPSDPLELVYTGTSVTPSRLETPSSVAEFSEATAELTVSFTNKVFT 240
D 181 YSFSSRDPLYLWSAPSDPLELVYTGTSVTPSRLETPSSVAEFSEATAELTVSFTNKVFT 240
QY 241 TETSRSTTSPKESDSPAGAPARQYTKGNLVRICTGAVILLLAGFLAEDWHSRRKRLRH 300
D 241 TETSRSTTSPKESDSPAGAPARQYTKGNLVRICTGAVILLLAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVGRPLPLPLPQTRKSHGGQDGGRCQDVHSRGLCS 339
D 301 RGRAVGRPLPLPLPQTRKSHGGQDGGRCQDVHSRGLCS 339
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RESULT 2

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US-10-157-031-387
Sequence 387, Application US/10157031
Publication No. US20030108890A1
GENERAL INFORMATION:
APPLICANT: Baranova, A. V.
APPLICANT: Yarkovsky, N. K.
APPLICANT: Kozlov, A. P.
APPLICANT: Jobashev, A. V.
APPLICANT: Krukovskaya, L. J.
TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
FILE REFERENCE: 2783-103
CURRENT APPLICATION NUMBER: US/10157,031
CURRENT FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 415
SOFTWARE: PatentIn version 3.1
SEQ ID NO 387
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
US-10-157-031-387
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Query Match 100.0% Score 1786; EH 15; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-139;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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D 1 MSPPTALFCLGLGRVPAQSGPLPKPSLQALPSSJVPLEKPVTLRCQGPFGVDLYRLE 60
QY 61 KLSSSRYQDQAVLFIPMKRSLAGRYRCSYQNGSLMSLPDQLELVATGVFAKPSLSAQP 120
D 61 KLSSSRYQDQAVLFIPMKRSLAGRYRCSYQNGSLMSLPDQLELVATGVFAKPSLSAQP 120
QY 121 GPAVSSGGDVTLCCQTRYGFDQALYKEGDPAPYKKNPERWYKASFPITVTAAHSGTYRC 180
D 121 GPAVSSGGDVTLCCQTRYGFDQALYKEGDPAPYKKNPERWYKASFPITVTAAHSGTYRC 180
QY 181 YSFSSRDPLYLWSAPSDPLELVYTGTSVTPSRLETPSSVAEFSEATAELTVSFTNKVFT 240
D 181 YSFSSRDPLYLWSAPSDPLELVYTGTSVTPSRLETPSSVAEFSEATAELTVSFTNKVFT 240
QY 241 TETSRSTTSPKESDSPAGAPARQYTKGNLVRICTGAVILLLAGFLAEDWHSRRKRLRH 300
D 241 TETSRSTTSPKESDSPAGAPARQYTKGNLVRICTGAVILLLAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVGRPLPLPLPQTRKSHGGQDGGRCQDVHSRGLCS 339
D 301 RGRAVGRPLPLPLPQTRKSHGGQDGGRCQDVHSRGLCS 339
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RESULT 3

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US-09-832-312-34
Sequence 34, Application US/09832312
Patent No. US20010049829A1
GENERAL INFORMATION:
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APPLICANT: Busfield et al.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-234
CURRENT APPLICATION NUMBER: US/09/832,312
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 34
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
US-09-832-312-34
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Query Match 99.8% Score 1782; DB 9; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.4e-139;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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D 61 KLSSSRYQDQAVLFIPMKRSLAGRYRCSYQNGSLMSLPDQLELVATGVFAKPSLSAQP 120
QY 121 GPAVSSGGDVTLCCQTRYGFDQALYKEGDPAPYKKNPERWYKASFPITVTAAHSGTYRC 180
D 121 GPAVSSGGDVTLCCQTRYGFDQALYKEGDPAPYKKNPERWYKASFPITVTAAHSGTYRC 180
QY 181 YSFSSRDPLYLWSAPSDPLELVYTGTSVTPSRLETPSSVAEFSEATAELTVSFTNKVFT 240
D 181 YSFSSRDPLYLWSAPSDPLELVYTGTSVTPSRLETPSSVAEFSEATAELTVSFTNKVFT 240
QY 241 TETSRSTTSPKESDSPAGAPARQYTKGNLVRICTGAVILLLAGFLAEDWHSRRKRLRH 300
D 241 TETSRSTTSPKESDSPAGAPARQYTKGNLVRICTGAVILLLAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVGRPLPLPLPQTRKSHGGQDGGRCQDVHSRGLCS 339
D 301 RGRAVGRPLPLPLPQTRKSHGGQDGGRCQDVHSRGLCS 339
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RESULT 4

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US-09-832-312-36
Sequence 36, Application US/09832312
Patent No. US20010049829A1
GENERAL INFORMATION:
APPLICANT: Busfield et al.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-234
CURRENT APPLICATION NUMBER: US/09/832,312
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 36
LENGTH: 339
TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-832-312-36

Query Match
Best Local Similarity 99.8%; Score 1782; DB 9; Length 339;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MSFSPALFCLGLGCRVPAOSGFLPKPSLQALPSSIVPLEKPYTLRCQGPFGVDLYRL 60
CY 61 KLSSTRYQDQAVLFIAPKRSLSAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQ 120
DB 61 KLSSTRYQDQAVLFIAPKRSLSAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQ 120
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DB 121 GPAVSSGGDVTLLQCQTRYGFDQFALYKGGDPAPYKNERWYRASFTITVTAHSGTYRC 180
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DB 181 YSFSSRDPLYLMSAPSDPLELVVTGTSVTPSRLPTPEPSSVAEFSEATAEITVSTNKVFT 240
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DB 241 TETSRSLTTSFKESDSPAGPARQVYTKGNLVRIICGAVILIIAGFLAEDWHSRRKRLRH 300
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DB 301 RGRAVGRPLPLPLPQTRKSHSGGDGGRQDVHSRGLCS 339

RESULT 5
US-09-832-312-38
; Sequence 38, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; PRIOR APPLICATION NUMBER: 2001-04-09
; PRIOR FILING DATE: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-38

Query Match
Best Local Similarity 99.8%; Score 1782; DB 9; Length 339;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1 MSFSPALFCLGLGCRVPAOSGFLPKPSLQALPSSIVPLEKPYTLRCQGPFGVDLYRL 60
DB 1 MSFSPALFCLGLGCRVPAOSGFLPKPSLQALPSSIVPLEKPYTLRCQGPFGVDLYRL 60
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DB 61 KLSSTRYQDQAVLFIAPKRSLSAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQ 120
CY 121 GPAVSSGGDVTLLQCQTRYGFDQFALYKGGDPAPYKNERWYRASFTITVTAHSGTYRC 180
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CY 181 YSFSSRDPLYLMSAPSDPLELVVTGTSVTPSRLPTPEPSSVAEFSEATAEITVSTNKVFT 240
DB 181 YSFSSRDPLYLMSAPSDPLELVVTGTSVTPSRLPTPEPSSVAEFSEATAEITVSTNKVFT 240
CY 241 TETSRSLTTSFKESDSPAGPARQVYTKGNLVRIICGAVILIIAGFLAEDWHSRRKRLRH 300
DB 241 TETSRSLTTSFKESDSPAGPARQVYTKGNLVRIICGAVILIIAGFLAEDWHSRRKRLRH 300
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DB 301 RGRAVGRPLPLPLPQTRKSHSGGDGGRQDVHSRGLCS 339
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US-09-832-312-40
; Sequence 40, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; PRIOR APPLICATION NUMBER: 2001-04-09
; PRIOR FILING DATE: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-40

Query Match
Best Local Similarity 99.8%; Score 1782; DB 9; Length 339;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1 MSFSPALFCLGLGCRVPAOSGFLPKPSLQALPSSIVPLEKPYTLRCQGPFGVDLYRL 60
DB 1 MSFSPALFCLGLGCRVPAOSGFLPKPSLQALPSSIVPLEKPYTLRCQGPFGVDLYRL 60
CY 61 KLSSTRYQDQAVLFIAPKRSLSAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQ 120
DB 61 KLSSTRYQDQAVLFIAPKRSLSAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQ 120
CY 121 GPAVSSGGDVTLLQCQTRYGFDQFALYKGGDPAPYKNERWYRASFTITVTAHSGTYRC 180
DB 121 GPAVSSGGDVTLLQCQTRYGFDQFALYKGGDPAPYKNERWYRASFTITVTAHSGTYRC 180
CY 181 YSFSSRDPLYLMSAPSDPLELVVTGTSVTPSRLPTPEPSSVAEFSEATAEITVSTNKVFT 240
DB 181 YSFSSRDPLYLMSAPSDPLELVVTGTSVTPSRLPTPEPSSVAEFSEATAEITVSTNKVFT 240
CY 241 TETSRSLTTSFKESDSPAGPARQVYTKGNLVRIICGAVILIIAGFLAEDWHSRRKRLRH 300
DB 241 TETSRSLTTSFKESDSPAGPARQVYTKGNLVRIICGAVILIIAGFLAEDWHSRRKRLRH 300
CY 301 RGRAVGRPLPLPLPQTRKSHSGGDGGRQDVHSRGLCS 339
DB 301 RGRAVGRPLPLPLPQTRKSHSGGDGGRQDVHSRGLCS 339

RESULT 7
US-10-446-826-5
; Sequence 5, Application US/10446826
; Publication No. US2003018685A1
```

GENERAL INFORMATION:

```

: APPLICANT: TANDON, NARENDRA N.
: APPLICANT: SUN, BING
: APPLICANT: NAKAMURA, TAKASHI
: APPLICANT: YAMAMOTO, NAOMASA
: TITLE OF INVENTION: PLATELET MEMBRANE GLYCOPROTEIN VI (GPVI) DNA AND
: TITLE OF INVENTION: PROTEIN SEQUENCES, AND USES THEREOF
: FILE REFERENCE: 03459, 0026-0000
: CURRENT APPLICATION NUMBER: US/10/446,826
: PRIOR FILING DATE: 2003-05-29
: PRIOR APPLICATION NUMBER: US/09/653,2553
: PRIOR FILING DATE: 2003-08-31
: PRIOR APPLICATION NUMBER: PCT/US00/23975
: PRIOR FILING DATE: 2000-09-01
: PRIOR APPLICATION NUMBER: 60/152,197
: PRIOR FILING DATE: 1999-09-01
: PRIOR APPLICATION NUMBER: 60/158,252
: PRIOR FILING DATE: 1999-10-08
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: Patent Ver. 2.1
: SEQ ID NO: 5
: LENGTH: 339
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-10-446-826-5

```

```

Query Match          96.5%; Score 1759; DB 12; Length 339;
Best Local Similarity 99.1%; Pred. No. 3,5e-137;
Matches 336; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

CY 1 MSPSPALFGLGICSRVPAQSGPLPKPSLQALPSLVLEKPVTLRCQPPGVLDYRL 60
DB 1 MSPSPALFGLGICSRVPAQSGPLPKPSLQALPSLVLEKPVTLRCQPPGVLDYRL 60
CY 61 KLSRRYQDQAVLETPAMKSLAGRYRCSYONGSLWSPSDQLELVATGVFAKSLSAQ 120
DB 61 KLSRRYQDQAVLETPAMKSLAGRYRCSYONGSLWSPSDQLELVATGVFAKSLSAQ 120
CY 121 GPVSSGGDVTJCCQTRYGFCQFALYKEGDPAPFKNERWYRASPPIITVAHSGTYRC 180
DB 121 GPVSSGGDVTJCCQTRYGFCQFALYKEGDPAPFKNERWYRASPPIITVAHSGTYRC 180
CY 181 YSPSRDPLVMSAPSDPLEVVTGTVTPSRLETPSSVAEFSBATLIVSFTNKVFT 240
DB 181 YSPSRDPLVMSAPSDPLEVVTGTVTPSRLETPSSVAEFSBATLIVSFTNKVFT 240
CY 241 TETSRITTSKESDSDPAGFAQYTKGNLVRICGAVIILAGFLAEDWHSRRKRLH 300
DB 241 TETSRITTSKESDSDPAGFAQYTKGNLVRICGAVIILAGFLAEDWHSRRKRLH 300
CY 301 RGRAVQAPLPPLPQTRKSHSGGQDGVHSRGLCS 339
DB 301 RGRAVQAPLPPLPQTRKSHSGGQDGVHSRGLCS 339

```

RESULT 8

US-09-832-312-5

Sequence 5, Application US/09832312

Patent No. US20010049829A1

GENERAL INFORMATION:

APPLICANT: Busfield et al.

TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF

FILE REFERENCE: 7853-234

CURRENT APPLICATION NUMBER: US/09/832,312

PRIOR FILING DATE: 2001-04-09

PRIOR APPLICATION NUMBER: 09/610,118

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: 09/503,387

PRIOR FILING DATE: 2000-02-14

PRIOR APPLICATION NUMBER: 09/454,824

PRIOR FILING DATE: 1999-12-06

PRIOR APPLICATION NUMBER: 09/345,468

PRIOR FILING DATE: 1999-06-30

NUMBER OF SEQ ID NOS: 78

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO: 5

LENGTH: 319

TYPE: PRT

ORGANISM: Homo sapiens

US-09-832-312-5

```

Query Match          94.0%; Score 1678; DB 9; Length 319;
Best Local Similarity 100.0%; Pred. No. 1.6e-130;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

CY 21 QSGPLPKPSLQALPSLVLEKPVTLRCQPPGVLDYRLKLSRRYQDQAVLETPAMK 80
DB 1 QSGPLPKPSLQALPSLVLEKPVTLRCQPPGVLDYRLKLSRRYQDQAVLETPAMK 80
CY 61 SLAGRYRCSYONGSLWSPSDQLELVATGVFAKSLSAQGPVSSGGDVTJCCQTRYGF 140
DB 61 SLAGRYRCSYONGSLWSPSDQLELVATGVFAKSLSAQGPVSSGGDVTJCCQTRYGF 140
CY 141 DQFALYKEGDPAPFKNERWYRASPPIITVAHSGTYRCYSPSRDPLVMSAPSDPLE 200
DB 121 DQFALYKEGDPAPFKNERWYRASPPIITVAHSGTYRCYSPSRDPLVMSAPSDPLE 180
CY 201 VVTGTVTPSRLETPSSVAEFSBATLIVSFTNKVFTTESRSITSPKESDSDPAG 260
DB 181 VVTGTVTPSRLETPSSVAEFSBATLIVSFTNKVFTTESRSITSPKESDSDPAG 240
CY 261 ARQYTKGNLVRICGAVIILAGFLAEDWHSRRKRLRHGRAVQAPLPPLPQTRK 320
DB 241 ARQYTKGNLVRICGAVIILAGFLAEDWHSRRKRLRHGRAVQAPLPPLPQTRK 300
CY 321 SHGGQDGVHSRGLCS 339
DB 301 SHGGQDGVHSRGLCS 319

```

RESULT 9

US-09-832-312-9

Sequence 5, Application US/09832312

Patent No. US20010049829A1

GENERAL INFORMATION:

APPLICANT: Busfield et al.

TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF

FILE REFERENCE: 7853-234

CURRENT APPLICATION NUMBER: US/09/832,312

PRIOR FILING DATE: 2001-04-09

PRIOR APPLICATION NUMBER: 09/610,118

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: 09/503,387

PRIOR FILING DATE: 2000-02-14

PRIOR APPLICATION NUMBER: 09/454,824

PRIOR FILING DATE: 1999-12-06

PRIOR APPLICATION NUMBER: 09/345,468

PRIOR FILING DATE: 1999-06-30

NUMBER OF SEQ ID NOS: 78

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO: 9

LENGTH: 249

TYPE: PRT

ORGANISM: Homo sapiens

US-09-832-312-9

```

Query Match          73.0%; Score 1304; DB 9; Length 249;
Best Local Similarity 100.0%; Pred. No. 8.7e-100;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

CY 21 QSGPLPKPSLQALPSLVLEKPVTLRCQPPGVLDYRLKLSRRYQDQAVLETPAMK 80
DB 1 QSGPLPKPSLQALPSLVLEKPVTLRCQPPGVLDYRLKLSRRYQDQAVLETPAMK 80
CY 81 SLAGRYRCSYONGSLWSPSDQLELVATGVFAKSLSAQGPVSSGGDVTJCCQTRYGF 140
DB 81 SLAGRYRCSYONGSLWSPSDQLELVATGVFAKSLSAQGPVSSGGDVTJCCQTRYGF 140

```

```
DB 61 SLAGRYRCSYQNGSLMSLPSDQLJLVATGVFAKPSLSAQPGPAVSSGGDVTLCQOTRYGF 120
QY 141 DQFALYKEDGPAPYKXPERWYRASFPITVTAHSGTYRCYSFSSSRDPYLSAPSDPLEJ 200
DB 121 DQFALYKEDGPAPYKXPERWYRASFPITVTAHSGTYRCYSFSSSRDPYLSAPSDPLEJ 180
QY 201 VWTGTSVTPSRLPTPEPSSVAEFSEATAELTVSFTNKVFTTETSRISITTSFKESDSPA 260
DB 181 VWTGTSVTPSRLPTPEPSSVAEFSEATAELTVSFTNKVFTTETSRISITTSFKESDSPA 240
QY 261 ARQYVTKGN 269
DB 241 ARQYVTKGN 249
```

RESULT 10

```
US-10-446-826-37
/ Sequence 37, Application US/10446826
/ Publication No. US20030186885A1
/ GENERAL INFORMATION:
/ APPLICANT: TANDON, NARENDRA N.
/ APPLICANT: SUN, BING
/ APPLICANT: NAKAMURA, TAKASHI
/ APPLICANT: YAMAMOTO, NAOKASA
/ TITLE OF INVENTION: PLATELET MEMBRANE GLYCOPROTEIN VI (GPVI): CNA AND
/ TITLE OF INVENTION: PROTEIN SEQUENCES, AND USES THEREOF
/ FILE REFERENCE: 03459-0026-00000
/ CURRENT APPLICATION NUMBER: US/10/446,826
/ PRIOR FILING DATE: 2003-05-29
/ PRIOR APPLICATION NUMBER: US/09/6593,255B
/ PRIOR FILING DATE: 2000-08-31
/ PRIOR APPLICATION NUMBER: PCT/US00/23975
/ PRIOR FILING DATE: 2000-09-01
/ PRIOR APPLICATION NUMBER: 60/152,197
/ PRIOR FILING DATE: 1999-09-01
/ PRIOR APPLICATION NUMBER: 60/159,251
/ PRIOR FILING DATE: 1999-10-08
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 37
/ LENGTH: 369
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-446-826-37
```

```
Query Match 73.0%; Score 1304; DB 12; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.5e-99;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 21 OSGLPKPSLQALPSSCVPLEKPVTLRCQGPQGVDPYRLEKLSSSRYPQDAVLPFAMKR 60
DB 98 QSGPLEKPSLQALPSSCVPLEKPVTLRCQGPQGVDPYRLEKLSSSRYPQDAVLPFAMKR 157
QY 81 SLAGRYRCSYQNGSLMSLPSDQLJLVATGVFAKPSLSAQPGPAVSSGGDVTLCQOTRYGF 140
DB 158 SLAGRYRCSYQNGSLMSLPSDQLJLVATGVFAKPSLSAQPGPAVSSGGDVTLCQOTRYGF 217
QY 141 DQFALYKEDGPAPYKXPERWYRASFPITVTAHSGTYRCYSFSSSRDPYLSAPSDPLEJ 200
DB 218 DQFALYKEDGPAPYKXPERWYRASFPITVTAHSGTYRCYSFSSSRDPYLSAPSDPLEJ 277
QY 201 VWTGTSVTPSRLPTPEPSSVAEFSEATAELTVSFTNKVFTTETSRISITTSFKESDSPA 260
DB 278 VWTGTSVTPSRLPTPEPSSVAEFSEATAELTVSFTNKVFTTETSRISITTSFKESDSPA 337
QY 261 ARQYVTKGN 269
DB 339 ARQYVTKGN 346
```

```
RESULT 11
US-09-832-312-16
/ Sequence 16, Application US/09832312
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```
/ Patent No. US20010049829A1
/ GENERAL INFORMATION:
/ APPLICANT: Busfield et al.
/ TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
/ FILE REFERENCE: 7853-234
/ CURRENT APPLICATION NUMBER: US/09/832,312
/ PRIOR FILING DATE: 2001-04-09
/ PRIOR APPLICATION NUMBER: 09/610,118
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: 09/503,397
/ PRIOR FILING DATE: 2000-02-14
/ PRIOR APPLICATION NUMBER: 09/454,824
/ PRIOR FILING DATE: 1999-12-06
/ PRIOR APPLICATION NUMBER: 09/345,468
/ PRIOR FILING DATE: 1999-06-30
/ NUMBER OF SEQ ID NOS: 78
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 16
/ LENGTH: 313
/ TYPE: PRT
/ ORGANISM: Mus musculus
/ US-09-832-312-16
```

```
Query Match 62.8%; Score 1122; DB 9; Length 313;
Best Local Similarity 69.4%; Pred. No. 1.3e-84;
Matches 218; Conservative 25; Mismatches 67; Indels 4; Gaps 2;
```

```
QY 1 XSPSPALFCGLCJGVPAQSGPULPKSLQALPSSVPLEKPVTLRCQGPQGVDPYRLE 59
DB 1 MSPASPTFCIGLCVQVYIQTQSGPLEKPSLQALPSSVPLEKPVTLRCQGPQGVDPYRLE 60
QY 60 EKLSSRYQDQAVLPFAMKPSLAGRYRCSYQNGSLMSLPSDQLJLVATGVFAKPSLSAQ 119
DB 61 EKLPEKEDQDPLFPTMERSNAGRYRCSYQNGSLMSLPSDQLJLVATGVFAKPSLSAQ 120
QY 120 PGPVSSGGDVTLCQOTRYGFQDQFALYKEDGPAPYKXPERWYRASFPITVTAHSGTYR 179
DB 121 PSSAVPQGDVTLKQGSYSPDFVLVYKGGTGPYKXPERWYRASFPITVTAHSGTYR 180
QY 180 CYSFSSSRDPYLSAPSDPLEJLVWTGTSVTPSRLPTPEPSSVAEFSEATAELTVSFTNKVF 239
DB 181 CYSFSSSRDPYLSAPSDPLEJLVWTGTSVTPSRLPTPEPSSVAEFSEATAELTVSFTNKVF 237
QY 240 TTETSRISITTSFKESDSPAQGPAPYKXPERWYRASFPITVTAHSGTYR 299
DB 238 TTEKPMNITASPEGLSPPIGFAMQHYAKGNLVRICLQATITILLGLAEDWHSRKKCLQ 297
QY 300 HRGAVQRPPLP 313
DB 298 HRMRALQRPPLP 311
```

```
RESULT 12
US-09-832-312-48
/ Sequence 48, Application US/09832312
/ Patent No. US20010049829A1
/ GENERAL INFORMATION:
/ APPLICANT: Busfield et al.
/ TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
/ FILE REFERENCE: 7853-234
/ CURRENT APPLICATION NUMBER: US/09/832,312
/ PRIOR FILING DATE: 2001-04-09
/ PRIOR APPLICATION NUMBER: 09/610,118
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: 09/503,397
/ PRIOR FILING DATE: 2000-02-14
/ PRIOR APPLICATION NUMBER: 09/454,824
/ PRIOR FILING DATE: 1999-12-06
/ PRIOR APPLICATION NUMBER: 09/345,468
/ PRIOR FILING DATE: 1999-06-30
/ NUMBER OF SEQ ID NOS: 78
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 48
```

LENGTH: 313
TYPE: prt
ORGANISM: Mus musculus
US-09-832-312-46

Query Match 62.8%; Score 1122; DB 9; Length 313;
Best Local Similarity 69.1%; Pred. No. 2.7e-84;
Matches 217; Conservative 25; Mismatches 67; Indels 4; Gaps 2;

QY 1 MSPPTALFCLGIC-LGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPFGVDLYRL 59
DB 1 MSPASPTFFCIGLCVLCVLTQSGPLPKPSLQALPSSLVPLGQSVILRCQGPFGVDLYRL 60
QY 60 EKISSSRVQDQAVLFIPAKKSLAGRYKCSYONGSLMSLPSDQLELVATGVPAKPSLSAQ 119
DB 61 EKIKPEKVEDQDFLPIFTMERSNAGRYKCSYONGSHMSLPSDQLELVATGVPAKPSLSAH 120
QY 120 PGPAVSSGGDVTLLCCQTRVGFDDQFALYKSGDPAPYKNEERWYRASFPITVTAAHSGTYR 179
DB 121 PSSAVPQGRDVTLLKQSPYSFDEFVLKESDTPGYKREKRYRANFPITVTAAHSGTYR 180
QY 180 CYSFSSRDPLYLMSAPSDLELVLTGTSVTPSRLPTFPSSVAEFSKATAEJTVSFTNKVF 239
DB 181 CYSFSSSSPYLMSAPSDPLVLTGTSATPSQVPTESFPVTSSRPSILP---TNKIS 237
QY 240 TTETSRSITTSFKESDSEAPGARQYVTKNVLVRCGAVILLIAGFLAEDMHSRKKLR 299
DB 236 TTEKYNITASPEGLSPFIQFAHQHYAKNVLVRCIGATITIIILGLAEDMHSRKKLCQ 297
QY 300 HGRGAVQRPPLP 313
DB 298 HRMRALQRPPLP 311

RESULT 13

US-09-832-312-42
Sequence 42, Application US/09832312
Patent No. US20010049829A1
GENERAL INFORMATION:
APPLICANT: Busfield et al.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7653-234
CURRENT APPLICATION NUMBER: US/09/832,312
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 42
LENGTH: 313
TYPE: prt
ORGANISM: Mus musculus
US-09-832-312-42

Query Match 62.6%; Score 1118; DB 9; Length 313;
Best Local Similarity 69.1%; Pred. No. 2.7e-84;
Matches 217; Conservative 25; Mismatches 68; Indels 4; Gaps 2;

QY 1 MSPPTALFCLGIC-LGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPFGVDLYRL 59
DB 1 MSPASPTFFCIGLCVLCVLTQSGPLPKPSLQALPSSLVPLGQSVILRCQGPFGVDLYRL 60
QY 60 EKISSSRVQDQAVLFIPAKKPSLAGRYKCSYONGSLMSLPSDQLELVATGVPAKPSLSAQ 119
DB 61 EKIKPEKVEDQDFLPIFTMERSNAGRYKCSYONGSHMSLPSDQLELVATGVPAKPSLSAH 120
QY 120 PGPAVSSGGDVTLLCCQTRVGFDDQFALYKSGDPAPYKNEERWYRASFPITVTAAHSGTYR 179

DB 121 PSSAVPQGRDVTLLKQSPYSFDEFVLKESDTPGYKREKRYRANFPITVTAAHSGTYR 180
QY 180 CYSFSSRDPLYLMSAPSDLELVLTGTSVTPSRLPTFPSSVAEFSKATAEJTVSFTNKVF 239
DB 181 CYSFSSSSPYLMSAPSDPLVLTGTSATPSQVPTESFPVTSSRPSILP---TNKIS 237
QY 240 TTETSRSITTSFKESDSEAPGARQYVTKNVLVRCGAVILLIAGFLAEDMHSRKKLR 299
DB 236 TTEKYNITASPEGLSPFIQFAHQHYAKNVLVRCIGATITIIILGLAEDMHSRKKLCQ 297
QY 300 HGRGAVQRPPLP 313
DB 298 HRMRALQRPPLP 311

RESULT 14

US-09-832-312-44
Sequence 44, Application US/09832312
Patent No. US20010049829A1
GENERAL INFORMATION:
APPLICANT: Busfield et al.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7653-234
CURRENT APPLICATION NUMBER: US/09/832,312
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 44
LENGTH: 313
TYPE: prt
ORGANISM: Mus musculus
US-09-832-312-44

Query Match 62.6%; Score 1118; DB 9; Length 313;
Best Local Similarity 69.1%; Pred. No. 2.7e-84;
Matches 217; Conservative 25; Mismatches 68; Indels 4; Gaps 2;

QY 1 MSPPTALFCLGIC-LGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPFGVDLYRL 59
DB 1 MSPASPTFFCIGLCVLCVLTQSGPLPKPSLQALPSSLVPLGQSVILRCQGPFGVDLYRL 60
QY 60 EKISSSRVQDQAVLFIPAKKSLAGRYKCSYONGSLMSLPSDQLELVATGVPAKPSLSAQ 119
DB 61 EKIKPEKVEDQDFLPIFTMERSNAGRYKCSYONGSHMSLPSDQLELVATGVPAKPSLSAH 120
QY 120 PGPAVSSGGDVTLLCCQTRVGFDDQFALYKSGDPAPYKNEERWYRASFPITVTAAHSGTYR 179
DB 121 PSSAVPQGRDVTLLKQSPYSFDEFVLKESDTPGYKREKRYRANFPITVTAAHSGTYR 180
QY 180 CYSFSSRDPLYLMSAPSDLELVLTGTSVTPSRLPTFPSSVAEFSKATAEJTVSFTNKVF 239
DB 181 CYSFSSSSPYLMSAPSDPLVLTGTSATPSQVPTESFPVTSSRPSILP---TNKIS 237
QY 240 TTETSRSITTSFKESDSEAPGARQYVTKNVLVRCGAVILLIAGFLAEDMHSRKKLR 299
DB 236 TTEKPMNITASPEGLSPFIQFAHQHYAKNVLVRCIGATITIIILGLAEDMHSRKKLCQ 297
QY 300 HGRGAVQRPPLP 313
DB 298 HRMRALQRPPLP 311

RESULT 15

US-09-832-312-46


```

Sequence 46, Application US/03832312
Patent No. US20010049829A1
GENERAL INFORMATION:
APPLICANT: Busfield et al.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-234
CURRENT APPLICATION NUMBER: US/09/832,312
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/610,119
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 46
LENGTH: 313
TYPE: PRT
ORGANISM: Mus musculus
US-09-832-312-46

```

```

Query Match 62.6%; Score 118; DE 9; Length 313;
Best Local Similarity 69.1%; Pred. No. 2,7e-84;
Matches 217; Conservative 25; Mismatches 68; Indels 4; Gaps 2;

```

```

CY 1 MSPSPALFCLGLC-LGRVPAQSGPLPKPSLQALPSSIVPLEKPVTLAQGPPVDLYR 59
DB 1 MSPASPTFCICGLCVLQVICTQSGPLPKPSLQALPSSIVPLEKPVTLAQGPPVDLYR 60
CY 60 EKLSSRYQDQAVLFTPMKESLAGRYKSYQNSLWSLPSDQJELVATGVFAKPSLSAQ 119
DB 61 EKLPEKYEEDQFLFTMERSNAGRYKCSYQNSHWSLPSDQJELIATGVYAKPSLSAH 120
CY 120 PGFAVSSGSDVTLQCCQRYGFDQFALYKGGPAPYKIPERNYKASFPYITVTAKSGTYR 179
DB 121 PSSAAPGGRDVTWKCCSPYSFDEPVLVYKGGTGPYKREKMYRANPPIITVTAKSGTYR 180
CY 180 CYSFSSRDPPYLSAPSDPLEVVTGTSTVPSRLPTSPSSVAEFSSEATNELTWSFTNKVF 239
DB 181 CYSFSSSSPYLWSAPSDPLVLTGSLATPSQVPTESFPVTSSRRPSILP---TNKIS 237
CY 240 TTETSRGITTSPKESDSPAGPARQYTKGNLVRICGAVILIIAGPFAECWHSRKRLR 299
DB 238 TTEKPKNITASPEGLSPYGFAGHQAQKNLVRICGATIIIIILGLAEQWHSRKKCLQ 297
CY 300 HSGRAVGRPPPLP 313
DB 298 HSMRALGRPPPLP 311

```

Search completed: October 23, 2003, 09:51:23
 Run time : 72 secs

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OM protein - protein search, using sw model

Run on: October 23, 2003, 11:35:00 ; Search time 20 Seconds
(without alignments)
717.169 Million cell updates/sec

Title: US-09-503-387-3
Perfect score: 1786
Sequence: 1 MSPSPFALFCLGLCLGRVPA.....KSHGQDGGQDVHSRGLCS 339

Scoring table: BLASTX62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310658 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/2/1aa/5A_CCM3.pep:*
2: /cgn2_6/prodata/2/1aa/5B_CCM3.pep:*
3: /cgn2_6/prodata/2/1aa/6A_CCM3.pep:*
4: /cgn2_6/prodata/2/1aa/6B_CCM3.pep:*
5: /cgn2_6/prodata/2/1aa/PCIVS_CCM3.pep:*
6: /cgn2_6/prodata/2/1aa/Backfile1.pep:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1786	100.0	339	US-09-345-468-3	Sequence 3, Appl
2	1786	100.0	339	US-09-414-453A-3	Sequence 3, Appl
3	1786	100.0	339	US-09-832-312-3	Sequence 3, Appl
4	1782	99.8	339	US-09-832-312-34	Sequence 34, Appl
5	1782	99.8	339	US-09-832-312-36	Sequence 36, Appl
6	1782	99.8	339	US-09-832-312-38	Sequence 38, Appl
7	1782	99.8	339	US-09-832-312-40	Sequence 40, Appl
8	1678	94.0	319	US-09-345-468-5	Sequence 5, Appl
9	1678	94.0	319	US-09-414-453A-5	Sequence 5, Appl
10	1678	94.0	319	US-09-832-312-5	Sequence 5, Appl
11	1304	73.0	249	US-09-414-453A-9	Sequence 9, Appl
12	1304	73.0	249	US-09-832-312-9	Sequence 9, Appl
13	1304	73.0	249	US-09-832-312-9	Sequence 9, Appl
14	1122	62.8	313	US-09-345-468-16	Sequence 16, Appl
15	1122	62.8	313	US-09-414-453A-16	Sequence 16, Appl
16	1122	62.8	313	US-09-832-312-16	Sequence 16, Appl
17	1122	62.8	313	US-09-832-312-18	Sequence 18, Appl
18	1118	62.6	313	US-09-832-312-42	Sequence 42, Appl
19	1118	62.6	313	US-09-832-312-44	Sequence 44, Appl
20	1118	62.6	313	US-09-832-312-46	Sequence 46, Appl
21	1080.5	60.5	292	US-09-345-468-18	Sequence 18, Appl
22	1080.5	60.5	292	US-09-414-453A-18	Sequence 18, Appl
23	1080.5	60.5	292	US-09-832-312-18	Sequence 18, Appl
24	937	52.5	267	US-09-345-468-19	Sequence 19, Appl
25	937	52.5	267	US-09-414-453A-19	Sequence 19, Appl
26	937	52.5	267	US-09-832-312-19	Sequence 19, Appl
27	498	27.9	448	US-09-310-463-18	Sequence 18, Appl

28	498	27.9	448	4	US-08-842-248A-18	Sequence 18, Appl
29	477	26.7	289	4	US-09-310-463-12	Sequence 12, Appl
30	477	26.7	289	4	US-08-842-248A-12	Sequence 12, Appl
31	455	25.5	299	4	US-09-310-463-30	Sequence 30, Appl
32	454	25.4	631	3	US-09-345-468-12	Sequence 12, Appl
33	454	25.4	631	4	US-09-414-453A-12	Sequence 12, Appl
34	454	25.4	631	4	US-09-832-312-12	Sequence 12, Appl
35	449	25.1	631	4	US-09-310-463-20	Sequence 20, Appl
36	449	25.1	631	4	US-08-842-248A-20	Sequence 20, Appl
37	441	24.7	483	4	US-09-310-463-16	Sequence 16, Appl
38	441	24.7	483	4	US-08-842-248A-16	Sequence 16, Appl
39	438.5	24.6	489	4	US-09-310-463-14	Sequence 14, Appl
40	438.5	24.6	489	4	US-08-842-248A-14	Sequence 14, Appl
41	438	24.5	431	3	US-09-985-950-14	Sequence 14, Appl
42	438	24.5	431	3	US-08-985-950-20	Sequence 20, Appl
43	438	24.5	431	4	US-09-546-049-14	Sequence 14, Appl
44	438	24.5	431	4	US-09-546-049-20	Sequence 20, Appl
45	434	24.3	598	4	US-09-310-463-10	Sequence 10, Appl

ALIGNMENTS

Result :
US-09-345-468-3
Sequence 3, Application US/05345468
Patent No. 6245527
GENERAL INFORMATION:
APPLICANT: Bustfield, S.
APPLICANT: Villavai, J.
APPLICANT: Jandrot-Perrus, M.
APPLICANT: Vainchenker, W.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-147
CURRENT APPLICATION NUMBER: US/09/345,468
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
US-09-345-468-3

Query Match: 100.0%; Score: 1786; DB 3; Length: 339;
Best Local Similarity: 100.0%; Pred. No. 8.3e-158;
Matches: 339; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY	1	MSPSPFALFCLGLCLGRVPAQSGPAPKPSLQALPSSLPVLEKPVTLRCQGPVGVYRL	60
DB	1	MSPSPFALFCLGLCLGRVPAQSGPAPKPSLQALPSSLPVLEKPVTLRCQGPVGVYRL	60
QY	61	KLSSRYQDQAVLFIFAMKRSLAGRYCSYQNGSLWSLPSDQLEVAATGVFAKPSLSAQF	120
DB	61	KLSSRYQDQAVLFIFAMKRSLAGRYCSYQNGSLWSLPSDQLEVAATGVFAKPSLSAQF	120
QY	121	GPAVSSGQVTLQCCRTYGFDFALYKGGDPAPYKMPERMYRASFPITVTAAHSGTYRC	180
DB	121	GPAVSSGQVTLQCCRTYGFDFALYKGGDPAPYKMPERMYRASFPITVTAAHSGTYRC	180
QY	181	YSPSSRDYPLMSAPDPLEJVTGTSVTFPSRLPTFPSSVAEFSEAATLTVSFTNKVFT	240
DB	181	YSPSSRDYPLMSAPDPLEJVTGTSVTFPSRLPTFPSSVAEFSEAATLTVSFTNKVFT	240
QY	241	TETSRITTSFKESDSFAGPARQYVTGNLVRIQAVLIIILAGLAEDWHSRRLRH	300
DB	241	TETSRITTSFKESDSFAGPARQYVTGNLVRIQAVLIIILAGLAEDWHSRRLRH	300
QY	301	RGAVQRPPLPLPPLPQTRKSHGQDGGQDVHSRGLCS	339
DB	301	RGAVQRPPLPLPPLPQTRKSHGQDGGQDVHSRGLCS	339

RESULT 2

US-09-414-453A-3

Sequence 3, Application US/09414453A
Patent No. 6383779

GENERAL INFORMATION:

APPLICANT: Busfield, S.

APPLICANT: Willeval, J.

APPLICANT: Jandrot-Petitus, M.

APPLICANT: Vainchenex, W.

TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF

FILE REFERENCE: 7853-147

CURRENT APPLICATION NUMBER: US/09/414,453A

CURRENT FILING DATE: 1999-10-07

PRIOR APPLICATION NUMBER: 09/345,468

PRIOR FILING DATE: 1999-06-30

NUMBER OF SEQ ID NOS: 24

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 3

LENGTH: 339

TYPE: PRT

ORGANISM: Homo sapiens

US-09-414-453A-3

Query Match 100.0%; Score 1766; DB 4; Length 339;

Best Local Similarity 100.0%; Pred. No. 8.3e-158;

Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MSPPTALFCLGLGRVPAQSGPLPKPSLQALFSSLVPLEKPTLRCCGPPGVLYRL 60

DB 1 MSPPTALFCLGLGRVPAQSGPLPKPSLQALFSSLVPLEKPTLRCCGPPGVLYRL 60

CY 61 KLSRRYQDQAVLFIPAKRSLAGRYRCSYONGSLWSLPSDQLELVATGVFAKPSLSAQ 120

DB 61 KLSRRYQDQAVLFIPAKRSLAGRYRCSYONGSLWSLPSDQLELVATGVFAKPSLSAQ 120

CY 121 GRAVSSGGDVTLCQCTRYGFDQFALYKEGDPAPYKNERMYRASFPITVTAHSGTYRC 180

DB 121 GRAVSSGGDVTLCQCTRYGFDQFALYKEGDPAPYKNERMYRASFPITVTAHSGTYRC 180

CY 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAEFTVFTNKVFT 240

DB 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAEFTVFTNKVFT 240

CY 241 TETSRSTTSPEKSDSPAGPARQYTKGNLVRIQLGAVITLLAGFLAEDHRRKRLRH 300

DB 241 TETSRSTTSPEKSDSPAGPARQYTKGNLVRIQLGAVITLLAGFLAEDHRRKRLRH 300

CY 301 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

DB 301 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

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CY 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

DB 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

LENGTH: 339

TYPE: PRT

ORGANISM: Homo sapiens

US-09-832-312-3

Query Match 100.0%; Score 1766; DB 4; Length 339;

Best Local Similarity 100.0%; Pred. No. 8.3e-158;

Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MSPPTALFCLGLGRVPAQSGPLPKPSLQALFSSLVPLEKPTLRCCGPPGVLYRL 60

DB 1 MSPPTALFCLGLGRVPAQSGPLPKPSLQALFSSLVPLEKPTLRCCGPPGVLYRL 60

CY 61 KLSRRYQDQAVLFIPAKRSLAGRYRCSYONGSLWSLPSDQLELVATGVFAKPSLSAQ 120

DB 61 KLSRRYQDQAVLFIPAKRSLAGRYRCSYONGSLWSLPSDQLELVATGVFAKPSLSAQ 120

CY 121 GRAVSSGGDVTLCQCTRYGFDQFALYKEGDPAPYKNERMYRASFPITVTAHSGTYRC 180

DB 121 GRAVSSGGDVTLCQCTRYGFDQFALYKEGDPAPYKNERMYRASFPITVTAHSGTYRC 180

CY 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAEFTVFTNKVFT 240

DB 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAEFTVFTNKVFT 240

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DB 241 TETSRSTTSPEKSDSPAGPARQYTKGNLVRIQLGAVITLLAGFLAEDHRRKRLRH 300

CY 301 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

DB 301 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

CY 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

DB 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

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DB 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

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DB 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

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DB 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

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DB 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

CY 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

DB 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

CY 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

DB 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

CY 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

DB 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

CY 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

DB 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

CY 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

DB 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

CY 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

DB 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

CY 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

DB 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

CY 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

DB 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

CY 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

DB 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

CY 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

DB 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

CY 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

DB 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

CY 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

DB 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

CY 339 RGRAVGRPLPPLPQTRKSHGCGDGRQDVHSRGLCS 339

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      |||
Db      121 GPAVSSGGDVTLQCCQTRYGFDQFALYKEDDPAPYKNERWYRASFDITVTAAHSQTYRC 180
      |||
QY      181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRPLTEPPSSVAEFSEATAEITVSTNKVFT 240
      |||
Db      181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRPLTEPPSSVAEFSEATAEITVSTNKVFT 240
      |||
QY      241 TETSRITTSFKESDSPAGPARQYTKGNLVRIICGAVILITLAGFLAEDWHSRRKRLRH 300
      |||
Db      241 TETSRITTSFKESDSPAGPARQYTKGNLVRIICGAVILITLAGFLAEDWHSRRKRLRH 300
      |||
QY      301 RGRAVQRPPLPPLPQTRKSHGGQDGRQDVHSRGJCS 339
      |||
Db      301 RGRAVQRPPLPPLPQTRKSHGGQDGRQDVHSRGJCS 339
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RESULT 5
US-09-832-312-36
; Sequence 36, Application US/09832312
; Patent No. 6548741
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,463
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-36

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Query Match      99.8%; Score 1782; DB 4; Length 339;
Best Local Similarity 99.7%; Pred. No. 2e-157;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 XSPSPALFELGLGCGRVPAQSGPLPKPSLQALPSSLVPLEKPVTRCQGFPGVDLYRLE 60
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Db      1 XSPSPALFELGLGCGRVPAQSGPLPKPSLQALPSSLVPLEKPVTRCQGFPGVDLYRLE 60
      |||
QY      61 KLSSSRYQDQAVLFIPAKKSLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQF 120
      |||
Db      61 KLSSSRYQDQAVLFIPAKKSLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQF 120
      |||
QY      121 GPAVSSGGDVTLQCCQTRYGFDQFALYKEDDPAPYKNERWYRASFDITVTAAHSQTYRC 180
      |||
Db      121 GPAVSSGGDVTLQCCQTRYGFDQFALYKEDDPAPYKNERWYRASFDITVTAAHSQTYRC 180
      |||
QY      181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRPLTEPPSSVAEFSEATAEITVSTNKVFT 240
      |||
Db      181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRPLTEPPSSVAEFSEATAEITVSTNKVFT 240
      |||
QY      241 TETSRITTSFKESDSPAGPARQYTKGNLVRIICGAVILITLAGFLAEDWHSRRKRLRH 300
      |||
Db      241 TETSRITTSFKESDSPAGPARQYTKGNLVRIICGAVILITLAGFLAEDWHSRRKRLRH 300
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QY      301 RGRAVQRPPLPPLPQTRKSHGGQDGRQDVHSRGJCS 339
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Db      301 RGRAVQRPPLPPLPQTRKSHGGQDGRQDVHSRGJCS 339
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RESULT 6
US-09-832-312-38

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; Sequence 38, Application US/09832312
; Patent No. 6548741
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,463
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-38

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Query Match      99.8%; Score 1782; DB 4; Length 339;
Best Local Similarity 99.7%; Pred. No. 2e-157;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 XSPSPALFELGLGCGRVPAQSGPLPKPSLQALPSSLVPLEKPVTRCQGFPGVDLYRLE 60
      |||
Db      1 XSPSPALFELGLGCGRVPAQSGPLPKPSLQALPSSLVPLEKPVTRCQGFPGVDLYRLE 60
      |||
QY      61 KLSSSRYQDQAVLFIPAKKSLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQF 120
      |||
Db      61 KLSSSRYQDQAVLFIPAKKSLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQF 120
      |||
QY      121 GPAVSSGGDVTLQCCQTRYGFDQFALYKEDDPAPYKNERWYRASFDITVTAAHSQTYRC 180
      |||
Db      121 GPAVSSGGDVTLQCCQTRYGFDQFALYKEDDPAPYKNERWYRASFDITVTAAHSQTYRC 180
      |||
QY      181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRPLTEPPSSVAEFSEATAEITVSTNKVFT 240
      |||
Db      181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRPLTEPPSSVAEFSEATAEITVSTNKVFT 240
      |||
QY      241 TETSRITTSFKESDSPAGPARQYTKGNLVRIICGAVILITLAGFLAEDWHSRRKRLRH 300
      |||
Db      241 TETSRITTSFKESDSPAGPARQYTKGNLVRIICGAVILITLAGFLAEDWHSRRKRLRH 300
      |||
QY      301 RGRAVQRPPLPPLPQTRKSHGGQDGRQDVHSRGJCS 339
      |||
Db      301 RGRAVQRPPLPPLPQTRKSHGGQDGRQDVHSRGJCS 339
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RESULT 7
US-09-832-312-40
; Sequence 40, Application US/09832312
; Patent No. 6548741
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,463
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 40
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
US-09-832-312-40

Query Match: 99.8%; Score 1678; DB 4; Length 339;
Best Local Similarity 99.8%; Pred. No. 29-157;
Matches 339; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY MSPPTALFCTGLGRLVNSGFLPKPSLQALPSSLVPLEKPYLRQGPVGLYLE 60
DB MSPPTALFCTGLGRLVNSGFLPKPSLQALPSSLVPLEKPYLRQGPVGLYLE 60
QY KLSRRYQDQAVLFIPAKNRSLACPRYQNSLMSVSSQGLVATGVFAKNSLSAOP 120
DB KLSRRYQDQAVLFIPAKNRSLACPRYQNSLMSVSSQGLVATGVFAKNSLSAOP 120
QY GFAVSSGGVTLQCCQTRVCFDQFALYKGGPAPYKNERWYRASPLITVTAHSGTYRC 180
DB GFAVSSGGVTLQCCQTRVCFDQFALYKGGPAPYKNERWYRASPLITVTAHSGTYRC 180
QY YSFSSRDYQWMSAPSDRELVTGTSTVTPSRPLTEPPSSVAEFSEATAEITVSEFNKVF 240
DB YSFSSRDYQWMSAPSDRELVTGTSTVTPSRPLTEPPSSVAEFSEATAEITVSEFNKVF 240
QY TETSRSTTSFKESDSPAGAPARQYTKNLVRIQAVLIIAGFLAEDWHSRKLPA 300
DB TETSRSTTSFKESDSPAGAPARQYTKNLVRIQAVLIIAGFLAEDWHSRKLPA 300
QY RGRAVQRPPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339
DB RGRAVQRPPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339

RESULT 8
US-09-345-468-5
Sequence 5; Application US/09345468
Patent No. 6245527
GENERAL INFORMATION:
APPLICANT: Busfield, S.
APPLICANT: Villaveal, J.
APPLICANT: Jandrot-Perrus, M.
APPLICANT: Vainchenker, W.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-147
CURRENT APPLICATION NUMBER: US/09/345,468
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 319
TYPE: PRT
ORGANISM: Homo sapiens
US-09-345-468-5

Query Match: 94.0%; Score 1678; DB 3; Length 319;
Best Local Similarity 100.0%; Pred. No. 8-1e-148;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY QSGPLPKPSLQALPSSLVPLEKPYLRQGPVGLYLEKLSRRYQDQAVLFIPAKNR 80
DB QSGPLPKPSLQALPSSLVPLEKPYLRQGPVGLYLEKLSRRYQDQAVLFIPAKNR 80
QY SLAGRYRCSYQNSLMSVSSQGLVATGVFAKNSLSAOPGPAVSSGGVTLQCCQTRVCF 140
DB SLAGRYRCSYQNSLMSVSSQGLVATGVFAKNSLSAOPGPAVSSGGVTLQCCQTRVCF 140
QY DQFALYKGGPAPYKNERWYRASPLITVTAHSGTYRCYFSFSSRDYQWMSAPSDREL 200
DB DQFALYKGGPAPYKNERWYRASPLITVTAHSGTYRCYFSFSSRDYQWMSAPSDREL 200
QY VTGTSTVTPSRPLTEPPSSVAEFSEATAEITVSEFNKVFETTSRSTTSFKESDSPAGP 260
DB VTGTSTVTPSRPLTEPPSSVAEFSEATAEITVSEFNKVFETTSRSTTSFKESDSPAGP 260

DB VTGTSTVTPSRPLTEPPSSVAEFSEATAEITVSEFNKVFETTSRSTTSFKESDSPAGP 260
QY ARQYTKGNLVRIQAVLIIAGFLAEDWHSRKLPAHGRAVQRPPLPPLPQTRK 320
DB ARQYTKGNLVRIQAVLIIAGFLAEDWHSRKLPAHGRAVQRPPLPPLPQTRK 320
QY SHGGQDGRQDVHSRGLCS 339
DB SHGGQDGRQDVHSRGLCS 339

RESULT 9
US-09-414-453A-5
Sequence 5; Application US/09414453A
Patent No. 6383779
GENERAL INFORMATION:
APPLICANT: Busfield, S.
APPLICANT: Villaveal, J.
APPLICANT: Jandrot-Perrus, M.
APPLICANT: Vainchenker, W.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-147
CURRENT APPLICATION NUMBER: US/09/414,453A
CURRENT FILING DATE: 1999-10-07
PRIOR APPLICATION NUMBER: 09/345,468
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 319
TYPE: PRT
ORGANISM: Homo sapiens
US-09-414-453A-5

Query Match: 94.0%; Score 1678; DB 4; Length 319;
Best Local Similarity 100.0%; Pred. No. 8-1e-148;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY QSGPLPKPSLQALPSSLVPLEKPYLRQGPVGLYLEKLSRRYQDQAVLFIPAKNR 80
DB QSGPLPKPSLQALPSSLVPLEKPYLRQGPVGLYLEKLSRRYQDQAVLFIPAKNR 80
QY SLAGRYRCSYQNSLMSVSSQGLVATGVFAKNSLSAOPGPAVSSGGVTLQCCQTRVCF 140
DB SLAGRYRCSYQNSLMSVSSQGLVATGVFAKNSLSAOPGPAVSSGGVTLQCCQTRVCF 140
QY DQFALYKGGPAPYKNERWYRASPLITVTAHSGTYRCYFSFSSRDYQWMSAPSDREL 200
DB DQFALYKGGPAPYKNERWYRASPLITVTAHSGTYRCYFSFSSRDYQWMSAPSDREL 200
QY VTGTSTVTPSRPLTEPPSSVAEFSEATAEITVSEFNKVFETTSRSTTSFKESDSPAGP 260
DB VTGTSTVTPSRPLTEPPSSVAEFSEATAEITVSEFNKVFETTSRSTTSFKESDSPAGP 260
QY ARQYTKGNLVRIQAVLIIAGFLAEDWHSRKLPAHGRAVQRPPLPPLPQTRK 320
DB ARQYTKGNLVRIQAVLIIAGFLAEDWHSRKLPAHGRAVQRPPLPPLPQTRK 320
QY SHGGQDGRQDVHSRGLCS 339
DB SHGGQDGRQDVHSRGLCS 339

RESULT 10
US-09-832-312-5
Sequence 5; Application US/09832312
Patent No. 654874
GENERAL INFORMATION:
APPLICANT: Busfield et al.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-234
CURRENT APPLICATION NUMBER: US/09/832,312

CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 319
TYPE: PRT
ORGANISM: Homo sapiens
US-09-832-312-5

Query Match 94.0%; Score 1678; DB 4; Length 319;
Best Local Similarity 100.0%; Pred. No. 9,1e-148;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 QSGPLPKPSJQALPSSLVPLEKPVTLRCQGPFGVDLYRLEKLSSTRYQDQAVLFPAVKR 90
DB 1 QSGPLPKPSJQALPSSLVPLEKPVTLRCQGPFGVDLYRLEKLSSTRYQDQAVLFPAVKR 90
QY 81 SLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGCVTLQCCQTRYGF 140
DB 61 SLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGCVTLQCCQTRYGF 120
QY 141 DQFALYKGGDPAPYKNERWYRASFPITVTAAHSGTYRCYSSSRDPYLSAPSDPLEL 200
DB 121 DQFALYKGGDPAPYKNERWYRASFPITVTAAHSGTYRCYSSSRDPYLSAPSDPLEL 180
QY 201 VVTGTSVTPSRLLPTPEPSSVAEFSEATLTLVSFTNKVFTTETSRITTSPKESDSPAGP 260
DB 181 VVTGTSVTPSRLLPTPEPSSVAEFSEATLTLVSFTNKVFTTETSRITTSPKESDSPAGP 240
QY 261 ARQYTTKGN 269
DB 241 ARQYTTKGNLVRIQLGAVLTLILAGFLAEDWHSRKRRLRRGRAVORLPLPLPQTRX 300

QY 321 SHGGQDGGROQVHSRGLCS 339
DB 301 SHGGQDGGROQVHSRGLCS 319

RESULT 11
US-09-345-468-9
Sequence 9, Application US/09345468
Patent No. 6245527
GENERAL INFORMATION:
APPLICANT: Busfield, S.
APPLICANT: Villavea, J.
APPLICANT: Jandrot-Petrus, M.
APPLICANT: Vainchenker, W.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-147
CURRENT APPLICATION NUMBER: US/09/345,468
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 249
TYPE: PRT
ORGANISM: Homo sapiens
US-09-345-468-9

Query Match 73.0%; Score 1304; DB 3; Length 249;
Best Local Similarity 100.0%; Pred. No. 3e-113;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 QSGPLPKPSJQALPSSLVPLEKPVTLRCQGPFGVDLYRLEKLSSTRYQDQAVLFPAVKR 80
DB 1 QSGPLPKPSJQALPSSLVPLEKPVTLRCQGPFGVDLYRLEKLSSTRYQDQAVLFPAVKR 80

DB 1 QSGPLPKPSJQALPSSLVPLEKPVTLRCQGPFGVDLYRLEKLSSTRYQDQAVLFPAVKR 90
QY 81 SLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGCVTLQCCQTRYGF 140
DB 61 SLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGCVTLQCCQTRYGF 120
QY 141 DQFALYKGGDPAPYKNERWYRASFPITVTAAHSGTYRCYSSSRDPYLSAPSDPLEL 200
DB 121 DQFALYKGGDPAPYKNERWYRASFPITVTAAHSGTYRCYSSSRDPYLSAPSDPLEL 180
QY 201 VVTGTSVTPSRLLPTPEPSSVAEFSEATLTLVSFTNKVFTTETSRITTSPKESDSPAGP 260
DB 181 VVTGTSVTPSRLLPTPEPSSVAEFSEATLTLVSFTNKVFTTETSRITTSPKESDSPAGP 240
QY 261 ARQYTTKGN 269
DB 241 ARQYTTKGN 249

RESULT 12
US-09-414-453A-9
Sequence 9, Application US/09414453A
Patent No. 6383779
GENERAL INFORMATION:
APPLICANT: Busfield, S.
APPLICANT: Villavea, J.
APPLICANT: Jandrot-Petrus, M.
APPLICANT: Vainchenker, W.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-147
CURRENT APPLICATION NUMBER: US/09/414,453A
CURRENT FILING DATE: 1999-10-07
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 249
TYPE: PRT
ORGANISM: Homo sapiens
US-09-414-453A-9

Query Match 73.0%; Score 1304; DB 4; Length 249;
Best Local Similarity 100.0%; Pred. No. 3e-113;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 QSGPLPKPSJQALPSSLVPLEKPVTLRCQGPFGVDLYRLEKLSSTRYQDQAVLFPAVKR 90
DB 1 QSGPLPKPSJQALPSSLVPLEKPVTLRCQGPFGVDLYRLEKLSSTRYQDQAVLFPAVKR 90
QY 81 SLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGCVTLQCCQTRYGF 140
DB 61 SLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGCVTLQCCQTRYGF 120
QY 141 DQFALYKGGDPAPYKNERWYRASFPITVTAAHSGTYRCYSSSRDPYLSAPSDPLEL 200
DB 121 DQFALYKGGDPAPYKNERWYRASFPITVTAAHSGTYRCYSSSRDPYLSAPSDPLEL 180
QY 201 VVTGTSVTPSRLLPTPEPSSVAEFSEATLTLVSFTNKVFTTETSRITTSPKESDSPAGP 260
DB 181 VVTGTSVTPSRLLPTPEPSSVAEFSEATLTLVSFTNKVFTTETSRITTSPKESDSPAGP 240
QY 261 ARQYTTKGN 269
DB 241 ARQYTTKGN 249

RESULT 13
US-09-832-312-9
Sequence 9, Application US/09832312
Patent No. 6548741
GENERAL INFORMATION:
APPLICANT: Busfield et al.

TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
 FILE REFERENCE: 7853-234
 CURRENT APPLICATION NUMBER: US/09/832,312
 CURRENT FILING DATE: 2001-04-09
 PRIOR APPLICATION NUMBER: 09/610,118
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: 09/503,387
 PRIOR FILING DATE: 2000-02-14
 PRIOR APPLICATION NUMBER: 09/454,824
 PRIOR FILING DATE: 1999-12-06
 PRIOR APPLICATION NUMBER: 09/345,468
 PRIOR FILING DATE: 1999-06-30
 NUMBER OF SEQ ID NOS: 78
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO: 5
 LENGTH: 249
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-832-312-9

Query Match 73.0%; Score 1104; DB 4; Length 249;
 Best Local Similarity 100.0%; Pred. No. 3e-113;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 QSGPLPKPS:QALPSSJVLKPVTLRCQGPVGVDJYRLKLSSSRYCQDAVLFEMKR 80
 DB 1 QSGPLPKPS:QALPSSJVLKPVTLRCQGPVGVDJYRLKLSSSRYCQDAVLFEMKR 80
 QY 81 SLAGRYRCYQNGSLMSLPSDQELVATGVFAKPSLSAOPGPAVSSGGDVTLCQCTRYGF 140
 DB 61 SLAGRYRCYQNGSLMSLPSDQELVATGVFAKPSLSAOPGPAVSSGGDVTLCQCTRYGF 120
 QY 141 DOFALYKESDPAPYKQPERVYRASPIITVTAAHSGTYRCYSSSRDPYLTMSAPSDPEL 200
 DB 121 DOFALYKESDPAPYKQPERVYRASPIITVTAAHSGTYRCYSSSRDPYLTMSAPSDPEL 180
 QY 201 VVTGTSVTPSRLETPSPSSVAESEAETVSTFNKVTETTSRSITTSPEKSDSPAGP 260
 DB 161 VVTGTSVTPSRLETPSPSSVAESEAETVSTFNKVTETTSRSITTSPEKSDSPAGP 240
 QY 261 ARQYTTKGN 269
 DB 241 ARQYTTKGN 249

RESULT 14
 US-09-345-468-16
 Sequence 16, Application US/09345468
 Patent No. 6245527
 GENERAL INFORMATION:
 APPLICANT: Busfield, S.
 APPLICANT: Villaveal, J.
 APPLICANT: Jandroot-Perrus, M.
 APPLICANT: Vainchenker, W.
 TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
 FILE REFERENCE: 7853-234
 CURRENT APPLICATION NUMBER: US/09/345,468
 CURRENT FILING DATE: 1999-06-30
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO: 16
 LENGTH: 313
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-345-468-16

Query Match 62.8%; Score 1122; DB 3; Length 313;
 Best Local Similarity 69.4%; Pred. No. 3.3e-96;
 Matches 218; Conservative 25; Mismatches 67; Indels 4; Gaps 2;

QY 60 EKLSSRYQDQAVLFIAPYKRSLAGRYRCYQNGSLMSLPSDQELVATGVFAKPSLSA 119
 DB 61 EKLKPEKYEEDQSLFIPTMERSNAGRYRCYQNGSLMSLPSDQELVATGVFAKPSLSA 120
 QY 120 PGPAVSSGGDVTLCQCTRYGFQDQALYKESDPAPYKQPERVYRASPIITVTAAHSGTYR 179
 DB 121 PGPAVSSGGDVTLCQCTRYGFQDQALYKESDPAPYKQPERVYRASPIITVTAAHSGTYR 180
 QY 180 CYSFSSSRDPYLTMSAPSDPELVTGTSVTPSRLETPSPSSVAESEAETVSTFNKVF 239
 DB 181 CYSFSSSRDPYLTMSAPSDPELVTGTSVTPSRLETPSPSSVAESEAETVSTFNKVF 237
 QY 240 TETSRSLTTSPEKSDSPAGPARYTKGNLVATGVFAKPSLSAOPGPAVSSGGDVTLCQCTRYGF 299
 DB 238 TETSRSLTTSPEKSDSPAGPARYTKGNLVATGVFAKPSLSAOPGPAVSSGGDVTLCQCTRYGF 297
 QY 300 HGRVAVQRPPLP 313
 DB 298 HGRVAVQRPPLP 311

RESULT 15
 US-09-414-453A-16
 Sequence 16, Application US/09414453A
 Patent No. 6383779
 GENERAL INFORMATION:
 APPLICANT: Busfield, S.
 APPLICANT: Villaveal, J.
 APPLICANT: Jandroot-Perrus, M.
 APPLICANT: Vainchenker, W.
 TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
 FILE REFERENCE: 7853-147
 CURRENT APPLICATION NUMBER: US/09/414,453A
 CURRENT FILING DATE: 1999-10-07
 PRIOR APPLICATION NUMBER: 09/345,468
 PRIOR FILING DATE: 1999-06-30
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO: 16
 LENGTH: 313
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-414-453A-16

Query Match 62.8%; Score 1122; DB 4; Length 313;
 Best Local Similarity 69.4%; Pred. No. 3.3e-96;
 Matches 218; Conservative 25; Mismatches 67; Indels 4; Gaps 2;

QY 1 MSPPTALFCLGIC-LGRVPAQSGPLPKPS:QALPSSJVLKPVTLRCQGPVGVDLYRL 59
 DB 1 MSPPTALFCLGIC-LGRVPAQSGPLPKPS:QALPSSJVLKPVTLRCQGPVGVDLYRL 50
 QY 60 EKLSSRYQDQAVLFIAPYKRSLAGRYRCYQNGSLMSLPSDQELVATGVFAKPSLSA 119
 DB 61 EKLKPEKYEEDQSLFIPTMERSNAGRYRCYQNGSLMSLPSDQELVATGVFAKPSLSA 120
 QY 120 PGPAVSSGGDVTLCQCTRYGFQDQALYKESDPAPYKQPERVYRASPIITVTAAHSGTYR 179
 DB 121 PGPAVSSGGDVTLCQCTRYGFQDQALYKESDPAPYKQPERVYRASPIITVTAAHSGTYR 180
 QY 180 CYSFSSSRDPYLTMSAPSDPELVTGTSVTPSRLETPSPSSVAESEAETVSTFNKVF 239
 DB 181 CYSFSSSRDPYLTMSAPSDPELVTGTSVTPSRLETPSPSSVAESEAETVSTFNKVF 237
 QY 240 TETSRSLTTSPEKSDSPAGPARYTKGNLVATGVFAKPSLSAOPGPAVSSGGDVTLCQCTRYGF 299
 DB 238 TETSRSLTTSPEKSDSPAGPARYTKGNLVATGVFAKPSLSAOPGPAVSSGGDVTLCQCTRYGF 297
 QY 300 HGRVAVQRPPLP 313
 DB 298 HGRVAVQRPPLP 311

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Job time : 21 secs